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(54) Title: INDUCTION OF CTL RESPONSES TO FOREIGN ANTIGENS EXPRESSED IN MYCOBACTERIA			
(57) Abstract			
<p>A method of inducing a CTL response in an animal which comprises administering to the animal mycobacteria transformed with at least one DNA sequence which encodes a protein or peptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes. The mycobacteria are administered in an amount effective to induce a CTL response in an animal. In one embodiment, the transforming DNA sequence may encode an HIV protein or fragment or derivative thereof.</p>			

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INDUCTION OF CTL RESPONSES TO FOREIGN ANTIGENS EXPRESSED IN MYCOBACTERIA

This invention relates to the induction of a T-cell response, in particular a cytotoxic T lymphocyte response. More particularly, this invention relates to the induction of CTL responses to proteins or polypeptides expressed by recombinant mycobacteria.

Cell-mediated immunity (or CMI) of infections is thought to be a major line of defense against certain infections, such as viral infections and certain bacterial infections. For example, CMI may be significant in the development of an effective vaccine against human immunodeficiency virus (HIV), or AIDS virus, because HIV vaccines and/or therapies based on the generation of passive transfer of HIV-specific antibody in the absence of cell-mediated immunity have not yielded consistent protection in primates challenged with the HIV virus. Thus, interest has turned to the induction of cell-mediated responses to various infections, such as for example, HIV infection, and to the identification of proteins or polypeptides that stimulate a cytotoxic T lymphocyte response, and to methods of administering such proteins or polypeptides.

In accordance with an aspect of the present invention, there is provided a method of inducing a CTL response in an animal comprising administering to the animal mycobacteria transformed with at least one DNA sequence which encodes a protein or peptide or fragment or derivative thereof which includes an epitope which

is recognized by cytotoxic T lymphocytes. The mycobacteria are administered in an amount effective to induce a CTL response in an animal.

Proteins or polypeptides for which the at least one DNA sequence may encode, include, but are not limited to, Mycobacterium leprae antigens; Mycobacterium tuberculosis antigens; Rickettsia antigens; Chlamydia antigens; Coxiella antigens; malaria sporozoite and merozoite proteins, such as the circumsporozoite protein from Plasmodium berghei sporozoites; Clostridium antigens; Leishmania antigens; Salmonella antigens; Mycobacterium africanum antigens; Mycobacterium intracellulare antigens; Mycobacterium avium antigens; E.coli antigens; Borrelia antigens; Listeria antigens; Francisella antigens; Yersinia antigens; Treponema antigens; Schistostoma antigens; Filaria antigens; Pneumococcus antigens; Staphylococcus antigens; Herpes virus antigens; influenza and parainfluenza virus antigens; measles virus antigens; mumps virus antigens; hepatitis virus antigens; Shigella antigens; Bordetella antigens; Hemophilus antigens; Streptococcus antigens; polio virus antigens; Rift Valley Fever virus antigens; dengue virus antigens; Human Immunodeficiency Virus (HIV) antigens; and respiratory syncytial virus (RSV) antigens.

In one embodiment, the at least one DNA sequence encodes at least one protein or polypeptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes induced by an HIV protein or fragment or derivative thereof. The at least one DNA sequence may encode an HIV protein or fragment or derivative thereof. HIV proteins or polypeptides which may be encoded by the at least one DNA sequence includes but are not limited to, HIV-I-gp 120; HIV-I-gp 41; HIV-I-gp 160; HIV-I-pol; HIV-I-nef; HIV-I-tat; HIV-I-rev; HIV-I-vif; HIV-I-vpr; HIV-I-vpu; HIV-I-gag; HIV-2-gp 120; HIV-2-gp 160; HIV-2-gp 41; HIV-2-gag; HIV-2-pol; HIV-2-nef;

HIV-2-tat; HIV-2-rev; HIV-2-vif; HIV-2-vpr; HIV-2-vpu; and HIV-2-vpx.

Mycobacteria which may be transformed with the at least one DNA sequence, which encodes a protein or polypeptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes, include, but are not limited to, Mycobacterium bovis-BCG, M. smegmatis, M. avium, M. phlei, M. fortuitum, M. lufu, M. paratuberculosis, M. habana, M. scrofulaceum, and M. intracellulare. In a preferred embodiment, the mycobacterium is M. bovis-BCG or a mutant thereof.

The at least one DNA sequence may be contained within an expression vector, which is transformed into a mycobacterium, whereby the mycobacterium expresses the protein or polypeptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes.

The expression vector may be, for example, a temperate shuttle phasmid or a bacterial-mycobacterial shuttle plasmid. Each of these vectors may be used to introduce the at least one DNA sequence encoding a protein or polypeptide or fragment or derivative which includes an epitope which is recognized by cytotoxic T lymphocytes, stably into mycobacteria, in which the at least one DNA sequence may be expressed. When a shuttle phasmid, which replicates as a plasmid in bacteria and a phage in mycobacteria, is employed, integration of the phasmid, which includes the at least one DNA sequence encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes, into the mycobacterial chromosome occurs through site-specific integration. The at least one DNA sequence which encodes a protein or polypeptide or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes, is replicated as part of the chromosomal DNA. When a bacterial-mycobacterial shuttle plasmid is employed, the at least one DNA sequence which encodes a protein or polypeptide or

fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes, is stably maintained extrachromosomally in a plasmid. Expression of the at least one DNA sequence occurs extrachromosomally (e.g., episomally). For example, the at least one DNA sequence is cloned into a shuttle plasmid and the plasmid is introduced into a mycobacterium such as those hereinabove described, wherein the plasmid replicates episomally. Examples of such shuttle plasmids and bacterial-mycobacterial shuttle plasmids are further described in Application Serial No. 361,944, filed June 5, 1989, which is hereby incorporated by reference.

In one embodiment the mycobacteria are transformed with an expression vector which comprises at least one DNA sequence encoding a protein or polypeptide which includes an epitope which is recognized by cytotoxic T lymphocytes, and a promoter selected from the class consisting of mycobacterial promoters and mycobacteriophage promoters for controlling expression of the DNA encoding the heterologous protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes.

Mycobacterial and mycobacteriophage promoters which may be employed include, but are not limited to, mycobacterial promoters such as the BCG HSP60 and HSP70 promoters; the mycobactin promoter from M. tuberculosis and BCG; the mycobacterial 14 kda and 12 kda antigen promoters; the mycobacterial α -antigen promoter from M. tuberculosis or BCG; the MBP-70 promoter, the mycobacterial 45 kda antigen promoter from M. tuberculosis or BCG; the superoxide dismutase promoter; the mycobacterial asd promoter, and mycobacteriophage promoters such as the Bxb1, L1, L5, and TM4 promoters. In one embodiment, the promoter is a mycobacterial heat shock protein promoter such as HSP60 or HSP70.

The promoter sequence may, in one embodiment, be part of an expression cassette which also includes a portion of the gene normally under the control of the promoter. For example, when a

mycobacterial HSP60 or HSP70 promoter is employed, the expression cassette may, within the scope of the present invention, include, in addition to the promoter, a portion of the gene for the HSP60 or HSP70 protein. When the expression cassette and the DNA encoding the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes are expressed, the protein expressed by the cassette and the DNA encoding the protein or polypeptide is a fusion protein of a fragment of a mycobacterial protein (eg., the HSP60 or HSP70 protein), and the protein or polypeptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes.

In a preferred embodiment, the transcription initiation site, the ribosomal binding site, and the start codon, which provides for the initiation of the translation of mRNA, are each of mycobacterial origin. The stop codon, which stops translation of mRNA, thereby terminating synthesis of the protein or polypeptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes, and the transcription termination site, may be of mycobacterial origin, or of other bacterial origin, or such stop codon and transcription termination site may be those of the DNA encoding the protein or polypeptide which includes an epitope which is recognized by cytotoxic T lymphocytes.

Preferably, the mycobacterial promoter is a BCG promoter, and the mycobacterium is BCG.

In one embodiment, the expression vector may further include DNA which encodes for proteins or polypeptides such as, but not limited to, antigens, anti-tumor agents, enzymes, lymphokines, pharmacologic agents, immunopotentiators, reporter molecules of interest in a diagnostic context, and selectable markers.

Selectable markers which may be encoded include, but are not limited to, the β -galactosidase marker, the kanamycin resistance

marker, the chloroamphenicol resistance marker, the neomycin resistance marker, and the hygromycin resistance marker.

In accordance with one embodiment, the vector further includes a mycobacterial origin of replication.

In accordance with another embodiment, the vector may be a plasmid. The plasmid may be a non-shuttle plasmid, or may be a shuttle plasmid which further includes a bacterial origin of replication such as an E.coli origin of replication, a Bacillus origin of replication, a Staphylococcus origin of replication, a Streptomyces origin of replication, or a pneumococcal origin of replication. In one embodiment, the shuttle plasmid includes an E. coli origin of replication.

In accordance with yet another embodiment, the vector may further include a multiple cloning site, and the DNA encoding for the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes is inserted in the multiple cloning site.

In addition to the DNA encoding a heterologous protein or polypeptide, and the mycobacterial promoter for controlling expression of the DNA encoding the protein or polypeptide which includes an epitope which is recognized by cytotoxic T lymphocytes, the expression vector may, in one embodiment, further include a DNA sequence encoding bacteriophage integration into a mycobacterium chromosome. Bacteriophages from which the DNA sequence encoding bacteriophage integration into a mycobacterium chromosome may be derived include, but are not limited to, mycobacteriophages such as but not limited to, the L5, L1, Bxb1, and TM4 mycobacteriophages; the lambda phage of E. coli; the toxin phages of Corynebacteria; phages of Actinomycetes and Norcardia; the ϕ C31 phage of Streptomyces; and the P22 phage of Salmonella. Preferably, the DNA sequence encodes mycobacteriophage integration into a mycobacterium chromosome. The DNA sequence which encodes bacteriophage integration into a mycobacterium chromosome may include DNA which encodes integrase,

which is a protein that provides for integration of the vector into the mycobacterial chromosome. Preferably, the DNA sequence encoding mycobacterial phage integration also includes DNA which encodes an attP site.

The DNA encoding the attP site and the integrase provides for an integration event which is referred to as site-specific integration. DNA containing the attP site and the integrase gene is capable of integrating into a corresponding attB site of a mycobacterium chromosome.

It is to be understood that the exact DNA sequence encoding the attP site may vary among different phages, and that the exact DNA sequence encoding the attB site may vary among different mycobacteria.

Examples of expression vectors which include mycobacterial promoters and mycobacteriophage promoters, for controlling the at least one DNA sequence encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes are further described in application Serial No. 642,017, filed January 16, 1991, which is a continuation of Application Serial No. 552,828, filed July 16, 1990, now abandoned. The contents of Application Serial No. 642,017 are hereby incorporated by reference.

In another embodiment, the mycobacteria are transformed with DNA which comprises a first DNA sequence which is a phage DNA portion encoding bacteriophage integration into a mycobacterium chromosome, and DNA including the at least one DNA sequence encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes.

The term "phage DNA portion", as used herein, means that the DNA sequence is derived from a phage and lacks the DNA which is required for phage replication.

Bacteriophages from which the phage DNA portion may be derived include, but are not limited to, mycobacteriophages, such

as but not limited to the those hereinabove described. Preferably, the phage DNA portion encodes mycobacteriophage integration into a mycobacterium chromosome.

In a preferred embodiment, the first DNA sequence includes DNA encoding integrase, which is a protein that provides for integration of the DNA into the mycobacterial chromosome. Most preferably, the first DNA sequence also includes DNA which encodes an AttP site.

The DNA sequence encoding the AttP site and the integrase provides for an integration event which is referred to as site-specific integration. DNA containing the AttP site and the integrase gene is capable of integration into a corresponding AttB site of a mycobacterium chromosome.

It is to be understood that the exact DNA sequence encoding the attP site may vary among different phages, and that the exact DNA sequence encoding the attB site may vary among different mycobacteria.

The integration event results in the formation of two new junction sites called AttL and AttR, each of which contain part of each of AttP and AttB. The inserted and integrated non-phage DNA which includes the first DNA sequence and the at least one DNA sequence, which encodes a protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes is flanked by the AttL and AttR sites. The insertion and integration of the phage DNA portion results in the formation of a transformed mycobacterium.

The DNA may further include DNA which encodes a selectable marker or markers; or other proteins or polypeptides of interest, such as, but not limited to anti-tumor agents, enzymes, lymphokines, pharmacologic agents, immunopotentiators, and reporter molecules of interest in a diagnostic context.

Selectable markers which may be encoded include, but are not limited to, the kanamycin resistance marker, the neomycin

resistance marker, the chloroamphenicol resistance marker, and the hygromycin resistance marker.

The phage DNA portion of the present invention, which includes the first DNA sequence encoding mycobacterium phage integration into a mycobacterium chromosome, and the at least one DNA sequence encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope recognized by cytotoxic T lymphocytes, may be constructed through genetic engineering techniques known to those skilled in the art. In a preferred embodiment, the phage DNA portion may be a plasmid including, in addition to the DNA encoding integration and the DNA encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope recognized by cytotoxic T lymphocytes, an origin of replication for any of a wide variety of organisms, which includes, but is not limited to, E.coli, Streptomyces species, Bacillus species, Staphylococcus species, Shigella species, Salmonella species and various species of pneumococci. Most preferably, the plasmid includes an origin of replication for E.coli.

The phage DNA portion also may include a suitable promoter. Suitable promoters include, but are not limited to, mycobacterial promoters and mycobacteriophage promoters such as those hereinabove described.

The promoter sequence may, in one embodiment, be part of an expression cassette which also includes a portion of the gene normally under the control of the promoter, as hereinabove described. For example, when a mycobacterial HSP60 or HSP70 promoter is employed, the expression cassette may include, in addition to the promoter, a portion of the gene for the HSP60 or HSP70 protein. When the expression cassette and the DNA encoding the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes are expressed, the protein expressed by the cassette and the DNA encoding the protein or polypeptide is a fusion

protein of a fragment of a mycobacterial protein (eg., the HSP60 or HSP70 protein), and the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes.

In a preferred embodiment, the transcription initiation site, the ribosomal binding site, and the start codon, which provides for the initiation of the translation of mRNA, are each of mycobacterial origin. The stop codon, which stops translation of mRNA, thereby terminating synthesis of the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes, and the transcription termination site, may be of mycobacterial origin, or of other bacterial origin, or such stop codon and transcription termination site may be those of the DNA encoding the protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes.

Examples of DNA which includes a first DNA sequence which is a phage DNA portion encoding bacteriophage integration into a mycobacterium chromosome, and DNA including the at least one DNA sequence encoding a protein or polypeptide, or fragment or derivative thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes are further described in application Serial No. 553,907, filed July 16, 1990, the contents of which are hereby incorporated by reference.

Mycobacteria which are transformed with DNA which encodes for a protein or polypeptide or fragment(s) or derivative(s) thereof, which includes an epitope which is recognized by cytotoxic T lymphocytes, may be employed in a composition, such as a vaccine, for inducing a CTL response in an animal. The vaccine may be administered to a human or non-human animal.

To form such a vaccine, the transformed mycobacteria are administered in conjunction with a suitable pharmaceutical carrier. As representative examples of suitable carriers there

may be mentioned: mineral oil, alum, synthetic polymers, etc. Vehicles for vaccines are well known in the art and the selection of a suitable vehicle is deemed to be within the scope of those skilled in the art from the teachings contained herein. The selection of a suitable vehicle is also dependent upon the manner in which the vaccine is to be administered. The vaccine may be in the form of an injectable dose and may be administered intramuscularly, intravenously, orally, intradermally, or by subcutaneous administration.

Other means for administering the vaccine or therapeutic agent should be apparent to those skilled in the art from the teachings herein; accordingly, the scope of the invention is not to be limited to a particular delivery form.

When the transformed mycobacteria are employed as a vaccine, such a vaccine has important advantages over other presently available vaccines. Mycobacteria have, as hereinabove indicated, adjuvant properties among the best currently known and, therefore, stimulate a recipient's immune system to respond with great effectiveness. This aspect of the vaccine induces cell-mediated immunity and thus is especially useful in providing immunity against pathogens in cases where cell-mediated immunity appears to be critical for resistance. Also, mycobacteria may stimulate long-term memory or immunity. It thus may be possible to prime long-lasting T cell memory, which stimulates secondary antibody responses neutralizing to the infectious agent. Such priming of T cell memory is useful, for example, against pertussis, malaria, influenza virus, Herpes virus, rabies, Rift Valley fever virus, dengue virus, measles virus, Human Immunodeficiency Virus (HIV), and respiratory syncytial virus.

The invention will now be described with respect to the following examples; however, the scope of the present invention is not to be limited thereby.

Example 1

A. Construction of plasmid including mycobacterial promoter expression cassette and lacZ gene.

1. Construction of pYUB125

Plasmid pAL5000, a plasmid which contains an origin of replication of M. fortuitum, and described in Labidi, et al., FEMS Microbiol. Lett., Vol. 30, pgs. 221-225 (1985) and in Gene, Vol. 71, pgs. 315-321 (1988), is subjected to a partial Sau 3A digest, and 5kb fragments are gel purified. A 5kb fragment is then ligated to Bam HI digested pIJ666 (an. E. coli vector containing an E. coli origin of replication and also carries neomycin-kanamycin resistance, as described in Kieser, et al., Gene, Vol. 65, pgs. 83-91 (1988) to form plasmid pYUB12. A schematic of the formation of plasmid pYUB12. A schematic of the formation of plasmid pYUB12 is shown in Figure 1. pYUB12 and pIJ666 were then transformed into M. smegmatis and BCG. Neomycin-resistant transformants that were only obtained by pYUB12 transformation confirmed that pAL5000 conferred autonomous replication to pIJ666 in M. smegmatis and BCG.

Shotgun mutagenesis by Snapper, et al (1988, hereinabove cited) indicated that no more than half of the pAL5000 plasmid was necessary to support plasmid replication in BCG. This segment presumably carried open reading frames ORF1 and ORF2, identified by Rauzier, et al., Gene, Vol. 71, pgs. 315-321 (1988), and also presumably carried a mycobacterial origin of replication. pYUB12 is then digested with HpaI and EcoRV, a 2586 bp carrying this region or segment pAL5000 is removed and ligated to PvuII digested pYUB8. Plasmid pYUB8 (a pBR322 derivative) includes an E. coli replicon and a kan^R (aph) gene. Ligation of the 2586 bp pYUB12 fragment to PvuII digested pYUB8 results in the formation of pYUB53, as depicted in Figure 2. Transformation of pYUB53 confirmed that the EcoRV-HpaI fragment, designated M.rep, was capable of supporting autonomous replication in BCG.

Plasmid pYUB53 was then digested with AatI, EcoRV, and PstI in order to remove the following restriction sites:

AatI 5707
EcoRI 5783
BamHI 5791
SalI 5797
PstI 5803
PstI 7252
SalI 7258
BamHI 7264
EcoRI 7273
ClaI 7298
HindIII 7304; and
EcoRV 7460

Fragment ends are then flushed with T4 DNA polymerase and religated to form plasmid pYUB125, construction of which is shown in Figure 3.

2. Elimination of superfluous vector DNA from pYUB125

792 bases of the tet gene, which had been inactivated by prior manipulations, was eliminated by a complete NarI digest, gel purification of the 6407 bp fragment, and ligation/recirculation, transformation of *E. coli* strain HB101, and selection of Kan^R transformants. The construction of resulting plasmid, pMV101, is schematically indicated in Figure 4, and the DNA sequence of pMV101, which includes markings of regions which will be deleted, and of mutations, as hereinafter described, is shown in Figure 5.

3. Construction of expression cassette based on BCG HSP60.

Among the most abundant proteins in mycobacteria is the HSP60 heat shock protein (also known as the 65 kda antigen). Because abundance of the HSP60 protein in mycobacteria indicates strong HSP60 gene expression, the sequence controlling HSP60 expression was chosen to control expression of heterologous genes encoding antigens or other proteins in BCG.

The published sequence of the BCG HSP60 gene (Thole, et al, Infect. and Immun., Vol. 55, pgs. 1466-1475 (June 1987)), and

surrounding sequence permitted the construction of a cassette carrying expression control sequences (i.e., promoter and translation initiation sequences) by PCR. The BCG HSP61 cassette (Figure 6) contains 375 bases 5' to the BCG HSP60 start codon, and 15 bases (5 codons) 3' to the start codon. PCR oligonucleotide primers were then synthesized. Primer Xba-HSP60, of the following sequence:

CAG ATC TAG ACG GTG ACC ACA ACG CGC C /

was synthesized for the 5' end of the cassette, and primer Bam-HSP61, of the following sequence:

CTA GGG ATC CGC AAT TGT CTT GGC CAT TG 2

was synthesized for the 3' end of the cassette. The primers were used to amplify the cassette by PCR from BCG strain Pasteur chromosomal DNA. The addition of the Bam HI site at the 3' end of the cassette adds one codon (Asp) to the first six codons of the HSP60 gene.

Each of pMV101 and the PCR cassette HSP61 was digested with NheI and BamHI. The PCR cassette was then inserted between the NheI and BamHI sites of pMV101, then ligated to form plasmid pMV65A (Figure 7).

The E. coli lac Z gene (Figure 8) was used as a reporter, or marker gene to assay the ability of the HSP61 cassette to express heterologous genes in BCG. A BamHI restriction fragment carrying the lac Z gene was cloned into the Bam HI site of Bam HI digested pMV65A, resulting in the formation of pMV65A/LZ as indicated schematically in Figure 7. The formation of pMV65A/LZ results in a fusion between the HSP60 and lac Z genes at the sixth codon of the HSP60 gene and the sixth codon of the lac Z gene. pMV65A/LZ was then transformed into E. coli. Blue E. coli colonies were selected on x-gal plates for the presence of pMV65A/LZ, thus indicating that the HSP60 promoter and translation initiation sequences were also active in E. coli.

pMV65A/LZ was then transformed into BCG and plated on Dubos Oleic Agar plates containing x-gal. All BCG colonies resulting

from this transformation exhibited blue color, thus indicating that the lac Z gene product (B-galactosidase) was expressed in BCG. SDS polyacrylamide gel electrophoresis was performed on lysates of the pMV65A/LZ BCG recombinants, revealing that B-galactosidase protein was expressed to levels in excess of 10% of total BCG protein (as determined by staining with Coomassie brilliant blue). These data indicated that BCG HSP61 expression cassette was functional in expression vector pMV65A.

Example 2

Cytotoxic T lymphocyte response to E. coli β -galactosidase.

E. coli β -galactosidase was expressed in BCG as a six amino acid fusion protein with BCG hsp 60 protein using extrachromosomal plasmid vector pMV65A/LZ utilizing the HSP60 promoter to drive expression. The recombinant BCG was grown to mid-log phase in Dubos media and concentrated by centrifugation. The bacteria were then re-suspended in PBS plus 0.05% Tween 80 and cup sonicated briefly to disperse clumped bacteria. Six week old BALB/c mice were inoculated with a single dose of 2×10^2 , 2×10^4 , or 2×10^6 colony forming units (CFU'S determined post-inoculation) by either intradermal (ID), intraperitoneal (IP), or intravenous (IV) injection. At 14 or 19 weeks post-immunization splenocytes were harvested from mice and CTL activity was measured. CTL activity was measured as follows:

Splenocytes (ACK-treated, 5×10^6 /ml) were stimulated in vitro in 10 ml in upright T25 flasks by co-culture for 5 days with mitomycin C-treated cells transfected with the lac Z gene (C3-4 cells; 5×10^6 /ml). A 4 hr. ^{51}Cr release assay was then performed in triplicate using P815 and P13.1 cells (P815 cells transfected with the lac Z gene) as targets. Various effector-target ratios were tested using 5,000 targets/well. Specific lysis was calculated as follows: % specific lysis = $100 \times [\text{release by effector cells minus spontaneous release} / \text{maximal release minus spontaneous release}]$.

At 19 weeks post-immunization, the remaining animals in each group were boosted by intraperitoneal injection at 10 µg of purified lac Z emulsified in incomplete Freund's adjuvant (IFA). Splenocytes were then harvested from these animals at 23 weeks and CTL activity was again measured. Unimmunized animals or animals immunized with lac Z emulsified in IFA, or animals immunized with vaccinia virus expressing lac Z served as controls.

The results of the above experiments, as determined by % specific lysis of target cells, indicated that a CTL response was induced in mice immunized with BCG transformed with the expression vector pMV65A/LZ.

Example 3

Construction of integrating plasmid including mycobacterial promoter expression cassette and HIV-I-gp 120 gene.

1. Elimination of undesirable restriction sites in aph (kan^R) gene.

To facilitate future manipulations, the HindIII and ClaI restriction sites in the aph gene in plasmid pMV101 were mutagenized simultaneously by polymerase chain reaction (PCR) mutagenesis according to the procedure described in Gene, Vol. 77 pgs. 57-59 (1989). The bases changed in the 'aph gene were at the third position of codons (wobble bases) within each restriction site and the base substitutions made were designed not to change the amino acid sequence of the encoded protein.

Separate PCR reactions of plasmid pMV101 with primer ClaMut-Kan + HindRMut-Kan and HindFMut-Kan + Bam-Kan were performed at 90°C (1 min.), 50°C (1 min.), and 72°C (1 min.) for 25 cycles. The PCR primers had the following base sequences:

ClaMut-Kan

CTT GTA TGG GAA GCC CC 3

HindRMut-Kan

GTG AGA ATG GCA AAA GAT TAT GCA TTT CTT TCC AG 5

HindFMut-Kan

GTG TGG AAA GAA ATG CAT AAT CTT TTG CCA TTC TCA CCG G 5'
Bam-Kan

CGT AGA GGA TCC AGA GGA CG 6

The resulting PCR products were gel purified and mixed and a single PCR reaction without primers was performed at 94°C (1 min.), 72°C (1 min.) for 10 cycles. Primers ClaMut-Kan and Bam-Kan were added and PCR was resumed at 94°C (1 min.), 50°C (1 min.), and 72°C (2 min.) for 20 cycles. The resulting PCR product (Kan. mut) was digested with BamHI and gel purified. Plasmid pMV101 was digested with ClaI and cohesive ends were filled in by Klenow + dCTP + dGTP. Klenow was heat inactivated and the digest was further digested with BamHI. The 5232 base pair fragment was gel purified and mixed with fragment Kan.mut and ligated. The ligation was transformed into E. coli strain HB101 and Kan^R colonies were screened for plasmids resistant to ClaI and HindIII digestion. Such plasmids were designated as pMV110, which is depicted in Figure 4.

2. Elimination of sequences not necessary for plasmid replication in mycobacteria.

Plasmid pMV110 was resected in separate constructions to yield plasmids pMV111 and pMV112. In one construction, pMV110 was digested with NarI and Ball, the ends were filled in, and a 5296 base pair fragment was ligated and recircularized to form pMV111. In another construct, pMV110 was digested with NdeI and SplI, the ends were filled in, and a 5763 base pair fragment was ligated and recircularized to form pMV112. Schematics of the constructions of pMV111 and pMV112 are shown in Figure 9. These constructions further eliminated superfluous E. coli vector sequences derived from pAL5000 not necessary for mycobacterial replication. Cloning was performed in E. coli. Plasmids pMV111 and pMV112 were tested for the ability to replicate in M. smegmatis. Because both plasmids replicated in M. smegmatis the deletions of each plasmid were combined to construct pMV113. (Figure 9).

To construct pMV113, pMV111 was digested with BamHI and EcoRI, and a 1071 bp fragment was isolated. pMV112 was digested with BamHI and EcoRI, and a 3570 bp fragment was isolated, and then ligated to the 1071 bp fragment obtained from pMV111 to form pMV113. These constructions thus defined the region of pAL5000 necessary for autonomous replication in mycobacteria as no larger than 1910 base pairs.

3.. Mutagenesis of restriction sites in mycobacterial replicon.

To facilitate further manipulations of the mycobacterial replicon, PCR mutagenesis was performed as above to eliminate the Sal I, EcoRI, and BglII sites located in the open reading frame known as ORF1 of pAL5000. PCR mutagenesis was performed at wobble bases within each restriction site and the base substitutions were designed not to change the amino acid sequence of the putative encoded ORF1 protein. The restriction sites were eliminated one at a time for testing in mycobacteria. It was possible to eliminate the SalI and EcoRI without altering replication in M. smegmatis. In one construction PCR mutagenesis was performed at EcoRI1071 of pMV113 with primers Eco Mut - M.rep and Bam-M.rep to form pMV117, which lacks the EcoRI1071 site. Primer Eco Mut - M.rep has the following sequence:

TCC GTG CAA CGA GTG TCC CGG A; 7

and Bam-M.rep has the following sequence:

CAC CCG TCC TGT GGA TCC TCT AC. 8

In another construction, PCR mutagenesis was performed at the SalI 1389 site with primer Sal Mut - M.rep and Bam-M.rep to form pMV119, which lacks the SalI 1389 site. Primer Sal Mut-M.rep has the following sequence:

TGG CGA CCG CAG TTA CTC AGG CCT. 9

pMV117 was then digested with ApaLI and BglII, and a 3360 bp fragment was isolated. pMV119 was digested with ApaLI and BglII, and a 1281 bp fragment was isolated and ligated to the 3360 bp fragment isolated from pMV117 to form pMV123. A schematic of the

constructions of plasmids pMV117, pMV119, and pMV123 is shown in Figure 10. Elimination of the BglII site, however, either by PCR mutagenesis or Klenow fill in, eliminated plasmid replication in mycobacteria, thus suggesting that the BglII site is in proximity to, or within a sequence necessary for mycobacteria plasmid replication.

4. Construction of pMV200 series vectors.

To facilitate manipulations of all the components necessary for plasmid replication in *E. coli* and mycobacteria, (*E. rep.* and *M. rep.*) and selection of recombinants (Kan^R), cassettes of each component were constructed for simplified assembly in future vectors and to include a multiple cloning site (MCS) containing unique restriction sites and transcription and translation terminators. The cassettes were constructed to allow directional cloning and assembly into a plasmid where all transcription is unidirectional.

Kan^R Cassette

A DNA cassette containing the aph (Kan^R) gene was constructed by PCR with primers Kan5' and Kan3'. An SpeI site was added to the 5' end of the PCR primer Kan3', resulting in the formation of a PCR primer having the following sequence:

CTC GAC TAG TGA GGT CTG CCT CGT GAA G. /O

BamHI + NheI sites were added to the 5' end of the primer Kan5', resulting in the formation of a PCR primer having the following sequence:

CAG AGG ATC CTT AGC TAG CCA CT GAC GTC GGG G. //

PCR was performed at bases 3375 and 4585 of pMV123, and BamHI and NheI sites were added at base 3159, and an SpeI site was added at base 4585. Digestion with BamHI and SpeI, followed by purification resulted in a 1228/2443 Kan^R cassette bounded by BamHI and SpeI cohesive ends with the direction of transcription for the aph gene proceeding from BamHI to Spe I.

E. rep. cassette

A DNA cassette containing the ColEI replicon of pUC19 was constructed by PCR with primers E.rep/Spe and E.rep/Mlu. An SpeI site was added to the 5' end of PCR primer E.rep/Spe and an MluI site was added to the 5' end of PCR primer E.rep/Mlu. The resulting primers had the following sequences:

E.rep./Spe

CCA CTA GTT CCA CTG AGC GTC AGA CCC 12

E.rep./Mlu

GAC AAC GCG TTG CGC TCG GTC GTT CGG CTG. 13

PCR was performed at bases 713 and 1500 of pUC19, and an MluI site was added to base 713, and a SpeI site was added to base 1500. Digestion with MluI and SpeI, followed by purification resulted in an E.rep. cassette bounded by SpeI and MluI cohesive ends with the direction of transcription for RNA I and RNA II replication primers proceeding from SpeI to MluI.

M.rep. cassette

A DNA cassette containing sequences necessary for plasmid replication in mycobacteria was constructed by PCR of pMV123 with primers M.rep/Mlu and M.rep/Bam. An MluI site was added to the 5' end of PCR primer M.rep/Mlu. A BamHI site was added to the 5' end of PCR primer M.rep/Bam. The resulting PCR primers had the following base sequences:

M.rep./Mlu

CCA TAC GCG TGA GCC CAC CAG CTC CG 14

M.rep./Bam

CAC CCG TCC TGT GGA TCC TCT AC 15

PCR was performed at bases 134 and 2082 of pMV123. An MluI site was added to base 2082. Digestion with BamHI and MluI, followed by gel purification resulted in a 1935 base pair DNA cassette bounded by MluI and BamHI cohesive ends with the direction of transcription for the pAL5000 ORF1 and ORF2 genes proceeding from MluI to Bam HI.

The Kan^R, E.rep, and M.rep PCR cassettes were then mixed in equimolar concentrations and ligated, and then transformed in E.

coli strain HB101 for selection of Kan^R transformants. Colonies were screened for the presence of plasmids carrying all three cassettes after digestion with BamHI + MluI + SpeI and designated pMV200. An additional restriction site, NcoI, was eliminated from the M.rep cassette by digestion of pMV200 with NcoI, fill in with Klenow, and ligation and recircularization, resulting in the formation of pMV201. A schematic of the formation of pMV200 from pMV123 and pUC19, and of pMV201 from pMV200, is shown in Figure 11. Plasmids pMV200 and pMV201 were transformed into M. smegmatis and BCG. Both plasmids yielded Kan^R transformants, thus indicating their ability to replicate in mycobacteria.

A synthetic multiple cloning sequence (MCS) (Figure 12) was then designed and synthesized to facilitate versatile molecular cloning and manipulations for foreign gene expressions in mycobacteria, and for integration into the mycobacterial chromosome. The synthetic MCS, shown in Figure 12, contains 16 restriction sites unique to pMV201 and includes a region carrying translation stop codons in each of three reading frames, and a transcription terminator derived from E. coli 5S ribosomal RNA (T1).

To insert the MCS cassette, pMV201 was digested with NarI and NheI, and the resulting fragment was gel purified. The MCS was digested with HinPI and NheI and, the resulting fragment was gel purified. The two fragments were then ligated to yield pMV204. A schematic of the construction of pMV204 is shown in Figure 13.

Plasmid pMV204 was then further manipulated to facilitate removal of the M.rep cassette in further constructions. pMV204 was digested with MluI, and an MluI - Not I linker was inserted into the MluI site between the M.rep and the E.rep to generate pMV206. A schematic of the construction of pMV206 from pMV204 is shown in Figure 14, and the DNA sequence of pMV206 is given in Figure 15.

5. Construction of expression cassette based on BCG HSP60.

The HSP61 cassette (Figure 6) was constructed as hereinabove described in Example 1.

Each of pMV206 and the PCR cassette HSP61 was digested with XbaI and BamHI. The PCR cassette was then inserted between the XbaI and BamHI sites of pMV206, then ligated to form plasmid pMV261. The construction of this plasmid is shown schematically in Figure 17. The reading frame and the restriction sites of the multiple cloning site of pMV261 is shown in Figure 16.

The E. coli lac Z gene was used as a reporter, or marker gene to assay the ability of the HSP61 cassette to express heterologous genes in BCG. A BamHI restriction fragment carrying the lac Z gene was cloned into the Bam HI site of Bam HI digested pMV261, resulting in the formation of pMV261/LZ. A schematic of the construction of pMV261/LZ is shown in Figure 18. The formation of pMV261/LZ results in a fusion between the HSP60 and lac Z genes at the sixth codon of the HSP60 gene and the sixth codon of the lac Z gene. pMV261/LZ was then transformed into E. coli. Blue E. coli colonies were selected on x-gal plates for the presence of pMV261/LZ, thus indicating that the HSP60 promoter and translation initiation sequences were also active in E. coli.

pMV261/LZ was then transformed into BCG and plated on Dubos Oleic Agar plates containing x-gal. All BCG colonies resulting from this transformation exhibited blue color, thus indicating that the lac Z gene product (B-galactosidase) was expressed in BCG. SDS polyacrylamide gel electrophoresis was performed on lysates of the pMV261/LZ BCG recombinants, revealing that B-galactosidase protein was expressed to levels in excess of 10% of total BCG protein (as determined by staining with Coomassie brilliant blue). These data indicated that BCG HSP61 expression cassette was functional in expression vector pMV261.

Plasmid pMV261/LZ was then shown to replicate autonomously, and express the E. coli B-galactosidase, or lacZ gene, driven by the BCG promoter HSP60, in M. smegmatis and BCG.

6. Transfer of mycobacteriophage L5 integration sequences to BCG expression vector.

Plasmid pMH9.4, which includes the mycobacteriophage L5 attP site, and the L5 integrase gene, was employed in providing the L5 integration sequences to a BCG expression vector. The construction of pMH9.4, as well as its integration into M. smegmatis and BCG, is described below in sections (i) through (vi).

(i) Identification of the DNA sequences of the attachment sites, attB, attL, and attR, of M. smegmatis.

Using standard technologies, a lambda EMBL3 library was constructed using chromosomal DNA prepared from mc²61 (a strain of M. smegmatis which includes an M. smegmatis chromosome into which has been integrated the genome of mycobacterial phage L5) and digested with Bam HI. Phage L5 contains DNA having restriction sites identical to those of phage L1 (Snapper, et al. 1988), except that L5 is able to replicate at 42°C and phage L1 is incapable of such growth. This library was then probed with a 6.7 kb DNA fragment isolated from the L5 genome that had been previously identified as carrying the attP sequence (Snapper, et al 1988). One of the positive clones was plaque purified, DNA prepared, and a 1.1 kb Sal I fragment (containing the AttL sequence) sub-cloned into sequencing vector pUC119. The DNA sequence of this fragment was determined using a shotgun approach coupled with Sanger sequencing. By isolating and sequencing the attL junction site and comparing this to the DNA sequence of L5 that was available, a region was determined where the two sequences aligned but with a specific discontinuity present. The discontinuity represents one side of a core sequence, which is identical in AttP, attB, and attL. The region containing the recombinational crossover point is shown in Figure 19.

The attL DNA (1.1 kb Sal I fragment) was used as a probe to hybridize to a Southern blot of Bam HI digested mc²6 DNA, which

is a strain of M. smegmatis which includes an M. smegmatis chromosome without any phage integration (Jacobs, et al, 1987, hereinabove cited.). A single band of approximately 6.4 kb was detected corresponding to the attB sequence of M. smegmatis. This same attL probe was used to screen a cosmid library of mc²⁶ (provided by Dr. Bill Jacobs of the Albert Einstein College of Medicine of Yeshiva University), and a number of positive cosmid clones were identified. DNA was prepared from these clones, and a 1.9 kb Sal I fragment (containing the attB site) that hybridizes to the attL probe was subcloned into pUC119 for sequencing and further analysis. The DNA sequence containing the core sequence was determined and is shown in Figure 19. The core sequence, which is identical in attP, attB and attL, has a length of 43bp.

The mc²⁶¹ lambda EMBL3 library was then probed with the 1.9kb SalI fragment containing the attB site. Positive plaques were identified, DNA was prepared, and analyzed by restriction analysis and Southern blots. Lambda clones were identified that contained a 3.2kb Bam HI fragment containing the putative attR site. The 3.2kb Bam HI fragment was purified and cloned into pUC119 for sequencing and further analysis.

(ii) Determination of attP-integrase region of L5 genome.

Concurrent with the above procedures, a significant portion of the DNA sequence of L5 had been determined and represented in several "contigs" or islands of DNA sequence. Sequences of the 6.7kb Bam HI fragment hereinabove described were determined by (a) analysis of the location of Bam HI sites in the contigs of the DNA of L5, and (b) by determining a short stretch of DNA sequence from around the Bam HI sites of plasmid pJR-1 (Figure 24), which carries the 6.7kb Bam HI fragment of L5.

A segment of DNA sequence was located that represented the 6.7kb Bam HI fragment of phage L5. Studies of other phages have shown that the integrase genes are often located close to the attP site. It was thus determined that the L5 integrase (int)

gene should lie either within the 6.7kb Bam HI fragment or in a DNA sequence on either side of it. The DNA sequence in the regions was then analyzed by translating it into all six possible reading frames and searching these amino acid sequences for similarity to the family of integrase related proteins, and through computer-assisted analysis of the DNA sequence. As shown in Figure 20, there are shown two domains of reasonably good conservation among L5 integrase and other integrases, and three amino acid residues that are absolutely conserved in domain 2. (See Yagil, et al., J. Mol. Biol., Vol. 207, pgs. 695-717 (1989), and Poyart-Salmeron, et al., J. EMBO., Vol. 8, pgs. 2425-2433 (1989)). A region was identified, and analysis of the corresponding DNA sequence showed a reading frame that could encode for a protein of approximately 333 amino acids. These observations identified the putative int gene.

The location of the int gene was not within the 6.7kb Bam HI fragment; however, it was very close to it with one of the Bam HI sites (that defines the 6.7kb Bam HI fragment) less than 100 bp upstream of the start of the gene. Analysis of the Bam HI sites showed that the int gene lay within a 1.9kb Bam HI fragment located adjacent to the 6.7kb Bam HI fragment. This 1.9kb Bam HI fragment was cloned by purification of the fragment from a Bam HI digest of L5 DNA and cloning into pUC 119, to generate pMH1 (Figure 25).

From a combination of the above approaches, a schematic of the organization of the attP-int region of L5 was constructed (Figure 26), and the gene sequence of the attP-int region is given in Figure 22.

(iii) Construction of pMH5.

The 6.7kb Bam HI fragment of mycobacteriophage L5, which contains the attP site, as hereinabove described, was cloned into the Bam HI site of pUC 119 (Figure 23). This was achieved by purifying the 6.7kb Bam HI fragment from a Bam HI digest of L5

DNA separated by agarose gel electrophoresis and ligating with Bam HI cut pUC 119. DNA was prepared from candidate recombinants and characterized by restriction enzyme analysis and gel electrophoresis. A recombinant was identified that contained the 6.7kb Bam HI fragment of L5 cloned into pUC 119. This plasmid was named pJR-1, as shown in Figure 24.

Analysis of DNA sequence data from a project to sequence L5 showed that a 1.9kb Bam HI fragment adjacent to the 6.7kb Bam HI fragment hereinabove described contained the integrase gene.

A plasmid containing a 1.9kb Bam HI fragment containing the DNA encoding for the integrase cloned into the Bam HI site of pUC 119 was constructed. The 1.9kb fragment was purified from a Bam HI digest of L5 DNA and cloned into the Bam HI site of pUC 119. Construction of the recombinant was determined by restriction analysis and gel electrophoresis. This plasmid was called pMH1, the construction of which is shown schematically in Figure 25.

pJR-1 was then modified by digestion with EcoRI and SnaBI (both are unique cloning sites), between which is a Bam HI site. The EcoRI-SnaBI fragment, including the Bam HI site was excised, and the plasmid was religated to form plasmid of pMH2, which contains on Bam HI site compared to two Bam HI sites contained in pJR-1. A schematic of the construction of pMH2 is shown in Figure 26.

The 1.9kb Bam HI fragment, which includes the integrase gene, was purified from a Bam HI digest of pMH1 and ligated to Bam HI digested pMH2. Recombinants were identified as above and the orientation of the 1.9kb fragment determined. A plasmid called pMH4 was thus constructed (Figure 27) in which the region from the Sna BI site (upstream of attP) through to the Bam HI site (downstream of the integrase gene) was identical to that in L5.

pMH4 was digested with HindIII (unique site) and was ligated to a 1kb HindIII fragment purified from pKD43 (supplied by Keith Darbyshire of the Nigel Gindley Laboratory) that contains the

gene determining resistance to kanamycin. Recombinants were identified and characterized as above. This plasmid is called pMH5. A schematic of the construction of pMH5 is shown in Figure 28.

(iv) Integration of pMH5 into attB of *M. smegmatis*.

Plasmids pYUB12 (a gift from Dr. Bill Jacobs, a schematic of the formation of which is shown in Figure 1), pMD01 (Figure 29), and pMH5 were electroporated, with four different concentrations of plasmid DNA over a 1,000-fold range, into *M. smegmatis* strain mc²155, a strain which is able to support plasmid replication. In sections (iv) through (vi), all electroporation procedures of *M. smegmatis*, or of BCG, were carried out as follows:

Cultures of organism were grown in Middlebrook 7H9 media, as described by Snapper, et al. (1988), harvested by centrifugation, washed three times with cold 10% glycerol, and resuspended at approximately a 100 x concentration of cells.

1 μ l of DNA was added to 100 μ l of cells in an ice-cold cuvette and pulsed in a Bio-Rad Gene Pulser, and given a single pulse at 1.25 kv at 25 μ F. 1 ml of broth was added the cells incubated for 1 hr. at 37°C for expression of the antibiotic-resistant marker. Cells were then concentrated and plated out on Middlebrook or tryptic soy media containing 15 μ g/ml kanamycin. Colonies were observed after 3 to 5 days incubation at 37°C.

Each of pYUB12, pMD01, and pMH5 carries kanamycin resistance. Plasmid pYUB12 carries an origin of DNA replication, while pMD01 lacks a mycobacterial origin of replication. Plasmid pMH5 does not carry a mycobacterial origin of replication, but carries a 2kb region of phage L5 which contains the attP site and the integrase gene (Figure 22). The number of transformants were linear with DNA concentration. Plasmid pYUB12 gives a large number of transformants (2×10^5 per μ g DNA) in mc²155, while pMH5 gives 6×10^4 transformants per μ g DNA, and pMD01 gives no transformants.

The above experiment was then repeated by electroporating the plasmids pYUB12, pMD01, and pMH5 into M. smegmatis strain mc²6, which does not support plasmid replication. No transformants in mc²6 were obtained from pYUB12 or pMD01, while pMH5 gave approximately 10⁴ kanamycin resistant transformants in mc²6 per µg of DNA, thus indicating integration of pMH5 into the mc²6 chromosome.

DNA from six independent pMH5 transformants (four in mc²155 and two in mc²6) was prepared. These DNA's (along with DNA from both mc²155 itself, and mc²155 carrying the plasmid pYUB12) were digested with a restriction enzyme, and analyzed by Southern blot and hybridization with the M. smegmatis 1.9kb attB probe hereinabove described. As shown in Figure 30, all six transformants have integrated into the attB site, resulting in the production of two new DNA fragments with different mobilities. If pMH5 did not integrate into the attB site, it would be expected that a single band, corresponding to the attB site in the mc²155 control, would be obtained.

(v) Construction of pMH9.2 and pMH9.4

pUC119 was digested with HindIII, and a 1kb HindIII fragment, containing a kanamycin resistance gene, purified from pKD43, was ligated to the HindIII digested pUC119 to form pMH8 (Figure 31). A 2kb SalI fragment (bp 3226-5310), which carries the attP and integrase gene from SalI digested pMH5, was purified and inserted in both orientations relative to the vector backbone of SalI digested pMH8 to form plasmids pMH9.2 and pMH9.4 (Figures 32 and 33).

M. smegmatis strain mc²155 cells carrying, as a result of electroporation, plasmid pYUB12, pMH9.2 or pMH9.4, or strain mc²6 cells carrying plasmid pMH5, as a result of electroporation as hereinabove described, were grown to saturation in broth with kanamycin. Cultures were then diluted 1:100 into broth without kanamycin and grown to saturation. Two further cycles of dilution and growth were done, corresponding to about 20

generations of bacterial growth. Cultures were plated out to single colonies on non-selective plates, and approximately 100 of these colonies were patch plated onto both non-selective and selective plates. The % of colonies that were sensitive to kanamycin, thus corresponding to the percentage of cells which lost the plasmid, is given below in Table I.

Table I

	<u>% loss</u>
pYUB12 (mc ² 155)	35
pMH5 (mc ² 6)	17
pMH9.2 (mc ² 155)	3
pMH9.4 (mc ² 155)	0

(vi) Transformation of BCG with pMH9.4

The 1.9 kb Sal I fragment, which includes the M. smegmatis attB site as hereinabove described was cloned into pUC119, and the plasmid generated was named pMH-12. (Figure 34).

Gel purified Sal I 1.9kb M. smegmatis fragment containing attB (isolated from pMH-12) was used to probe a Southern transfer of Bam HI digested mycobacterial DNA's, including BCG substrain Pasteur, shown in Figure 35. This demonstrated that there is one Bam HI fragment of BCG that strongly hybridizes to the M. smegmatis attB probe and three hybridize weakly. The strongest hybridizing band is the fastest moving band (approximately 1.9 kb).

The same probe as above was used to probe a BCG cosmid library (provided by Dr. Bill Jacobs) and positive clones were identified. DNA was prepared from several positive clones and analyzed by restriction analysis and Southern blotting. The 1.9 kb Bam HI fragment (corresponding to the strongly hybridizing band in the Southern blot was identified, gel purified from the cosmid DNA and cloned into pUC119. The resulting plasmid was named pMH-15. (Figure 36).

Plasmid pMH-5 and pMH9.4 were electroporated into BCG Pasteur. It was observed that pMH9.4 transforms BCG with high

efficiency (approximately 10^4 transformants/ μ g DNA), while pMH-5 transforms BCG at low efficiency (1-10 transformants/ μ g DNA). DNA was prepared from BCG transformants and analyzed by Bam HI restriction and Southern blot analysis, probing with gel purified 1.9kb Bam HI BCG attB fragment from pMH-15. These data are shown in Figure 37 and show that integration of both pMH5 and pMH9.4 is specific to the BCG attB site (ie. the strongly cross-hybridizing fragment in BCG). This is illustrated by the loss of the 1.9kb Bam HI fragment from the transformants and the appearance of two new bands representing attL and attR junction fragments. Figure 37 shows just one of the pMH5/BCG transformants, although all of the four that were analyzed show that one of the bands (the largest) is smaller than expected (and different in each of the transformants), indicating that the transformation efficiency of pMH-5 is low in BCG. In contrast, the four pMH9.4 transformants are identical to each other (Figure 37) and give attR and attL junction fragments of the predicted sizes.

Plasmid pMH9.4, which includes the mycobacterial phage L5 attP site and the L5 integrase gene, was digested to completion with either KpnI + PvuII or XbaI + PvuII, and a restriction fragment of 1862 or 1847 base pairs, respectively, each of which contain the attP site and the integrase gene, were purified by agarose gel electrophoresis. Plasmid pMV261/LZ was digested with XbaI or DraI to generate either a 7569 bp or 7574 bp vector fragment. The 7569 bp fragment was ligated to the 1862 bp fragment derived from pMH9.4 to form pMV460/LZ. The 7574 bp fragment was ligated to the 1847 bp fragment derived from pMH9.4 to form pMV460 R/LZ. Plasmids pMV460 F/LZ and pMV460R/LZ each include a mycobacterial replicon, the L5 attP site, and the L5 integrase gene. A schematic of the formation of plasmids pMV460 F/LZ and pMV460R/LZ is shown in Figure 38. To generate derivatives without the mycobacterial plasmid replicon, plasmids pMV460/LZ and pMV460R/LZ were digested with NotI and recircularized by ligation to generate pMV360F/LZ and pMV360R/LZ.

A schematic of the construction of pMV360F/LZ and pMV360R/LZ is shown in Figure 39.

Plasmids pMH9.4, pMV261/LZ, pMV460/LZ, pMV460/LZ, pMV460/LZ, and pMV460/LZ were then transformed into M. smegmatis and BCG to test their ability to replicate autonomously or integrate into the M. smegmatis or the BCG chromosome. Transformation with pMH9.4, pMV261/LZ, pMV360F/LZ, and pMV360R/LZ yielded kanamycin resistant transformants of M. smegmatis and BCG. Transformants of pMV261LZ, pMV360F/LZ, and pMV360R/LZ were shown to express E. coli B-galactosidase by SDS-polyacrylamide gel electrophoresis and X-gal assay. Plasmids pMV460F/LZ and pMV460R/LZ failed to yield kanamycin resistant transformants, thus indicating that chromosomal integration of a plasmid carrying sequences mediating autonomous replication is lethal to mycobacteria.

7. Construction of pMV307.

Plasmid pMV206 was digested with NotI to remove the mycobacterial replicon. The resulting 2209 bp fragment, which includes the aph (Kan^R) gene, the E. coli replicon and the multiple cloning site, was ligated and recircularized to form pMV205, the construction of which is schematically depicted in Figure 14.

PCR with primers XbaI-Att/Int and NheI-Att/Int was then performed on a Sal I fragment from pMH9.4, which contains the attP site and the L5 integrase gene. The resulting cassette was then digested with XbaI and NheI and a 1789 bp fragment was gel purified. pMV205 was then digested with NheI, and the resulting fragment was ligated to the 1989 bp fragment obtained from pMH9.4 to form pMV307. A schematic of the construction of pMV307 is shown in Figure 40.

8. Construction of pMV261/HIV1-gp 120.

An SmaI-ClaI antigen gene fragment, or cassette, was constructed by PCR, and cloned between the Bam HI and ClaI restriction sites of pMV261 to form pMV261/HIV1-gp 120.

Plasmid pMV261/HIV1-gp 120 was transformed into BCG, and the presence of the corresponding antigen in BCG was verified by the appearance of immunoreactive protein bands in Western blot analysis of BCG recombinant lysates.

9. Construction of pMV361/HIV1-gp 120

The HIV1-gp 120 antigen gene expression cassette, which includes a promoter sequence and an HIV1-gp 120 gene sequence, was excised from the pMV261 derivatives with NotI and a second restriction enzyme site (Pvu II, Eco RI, Sal I, Cla I or Hind III) and cloned into the integrating plasmid pMV307 between the NotI site and a second enzyme site (Pvu II, Eco RI, Sal I, Cla I or Hind III) to form the plasmid pMV361/HIV-Igpl20. The backbone of this plasmid is shown in Figure 41.

Plasmid pMV361/HIV-Igpl20 was transformed into BCG and shown to express the corresponding antigens by Western blot analysis (Figure 42) with the appropriate antigen-specific human sera.

Example 4

Cytotoxic T lymphocyte responses to HIV-1-gp 120

HIV-1 gp 120 was expressed in BCG as a six amino acid fusion protein with BCG hsp 60 protein using vector pMV361/HIV-1-gp120, using the hsp 60 promoter to control expression.

Two groups of mice were inoculated with 1×10^6 CFU's of recombinant BCG expressing the gp 120 gene from the integrative plasmid pMV361/HIV-1-gp120. One group received the BCG via intraperitoneal injection (100 ul) whereas the other group received the BCG by deposition of the dose (10 ul) rubbed into a tail scratch.

CTL activity was measured at various times after immunization. CTL activity was measured as follows:

Two mice from each group were sacrificed at various times after immunation, and the spleens were removed. Single cell suspensions were made and the red blood cells were lysed with ammonium chloride. The cells were stimulated in vitro for 5 days with P815 cells that were pulsed with peptide P18, a fifteen

residue synthetic peptide within HIV1-gp 120. A 4-hour chromium (Cr^{51}) release assay was then carried out using untreated P815 and peptide P18 pulsed P815 cells as targets. Significant P18-specific CTL activity was observed in the mice immunized by tail scratch 14 weeks after immunization. At 16 weeks, CTL activity was observed in both groups of mice. Upon repeat of this experiment, CTL activity was observed at time points as early as 8 weeks after immunization.

Example 5

Recombinant BCG transformed with pMV361/HIV1-gp 120 were grown to mid-log phase in Dubos media and concentrated by centrifugation. The bacteria were then resuspended in 15% glycerol and frozen using a rate controlled freezing apparatus. The bacteria were stored at -70°C until use (referred to as "vaccine"). A second preparation grown in the same way was not frozen and is referred to as a "fresh" preparation. Prior to immunization of animals, the bacteria were resuspended in PBS + 0.05% Tween 80 to the desired concentration and cup sonicated briefly to disperse clumped bacteria. Six week old BALB/c mice were inoculated with a single dose of 5×10^4 cfu fresh bacteria (determined post inoculation) or 1.5×10^5 frozen bacteria (determined pre-inoculation) by tail scratch (t.s.) injection. At 8 weeks post-immunization, splenocytes were harvested from animals and CTL activity was measured (described below). Splenocytes from unimmunized animals were used as controls in the CTL assays.

CTL activity was determined as follows:

Splenocytes (ACK-treated, $5 \times 10^6/\text{ml}$) were stimulated in vitro in 10 ml in upright T25 flasks by co-culture for 5 days with mitomycin C-treated P815 cells ($5 \times 10^6/\text{ml}$) that were pulsed with 250 ug/ml of peptide P18 for one hour. A 4 hr. ^{51}Cr release assay was subsequently performed in triplicate using P815 targets with or without pulsing for 1 hour with 250 ug/ml peptide P18. Various effector-target ratios were tested using 5000

targets/well. Specific lysis was calculated as follows: % specific lysis = $100 \times [\text{release by effector cells} - \text{spontaneous release}] / [\text{maximal release} - \text{spontaneous release}]$.

The results are given in Figure 42.

As shown in Figure 43, both groups of mice showed an increased CTL response at 8 weeks after immunization as compared with unimmunized mice.

Example 6

Recombinant BCG transformed with pMV361/HIV1-gp 120. were grown to mid-log phase in Dubos media and concentrated by centrifugation. The bacteria were then resuspended in 15% glycerol and frozen using a rate controlled freezing apparatus. The bacteria were stored at -70°C until use (referred to as "vaccine"). A second preparation grown in the same way was not frozen and is referred to as a "fresh" preparation. Prior to immunization of animals, the bacteria were resuspended in PBS + 0.05% Tween 80 to the desired concentration and cup sonicated briefly to disperse clumped bacteria. Six week old BALB/c mice were inoculated with a single dose of 5×10^4 cfu fresh bacteria (determined post inoculation) or 1.5×10^5 frozen bacteria (determined pre-inoculation) by tail scratch (t.s.) injection. At 8 weeks post-immunization, splenocytes were harvested from animals and CTL activity was measured (described below).

CTL activity was determined as follows:

Lymph node cells ($5 \times 10^6/\text{ml}$) were stimulated in vitro in 10 ml in upright T25 flasks by co-culture for 5 days with mitomycin C-treated P815 cells ($5 \times 10^6/\text{ml}$) that were pulsed with 250 ug/ml of peptide P18 for one hour. A 4 hr ^{51}Cr release assay was subsequently performed in triplicate using P815 (matched) or EL4 (mismatched) targets with or without pulsing for 1 hour with 250 ug/ml peptide P18. Various effector target ratios were tested using 5000 targets/well. Specific lysis was calculated as follows: % specific lysis = $100 \times [\text{release by effector cells} - \text{spontaneous release}] / [\text{maximal release} - \text{spontaneous release}]$.

minus spontaneous release/maximal release minus spontaneous release].

The results of this assay are given in Figure 44.

As shown in Figure 44, a CTL response to HIV-1 gp 120 using lymph node cells was demonstrated following immunization of mice with BCG transformed with pMV361/HIV-1 gp 120.

It is to be understood, however, that the scope of the present invention is not to be limited to the specific embodiments described above. The invention may be practiced other than as particularly described and still be within the scope of the accompanying claims.

WHAT IS CLAIMED IS:

1. A method of inducing a CTL response in an animal comprising:

administering to an animal mycobacteria transformed with at least one DNA sequence which encodes a protein or peptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes, said mycobacteria being administered in an amount effective to induce a CTL response in an animal.

2. The method of Claim 1 wherein said protein or peptide or fragment or derivative thereof includes an epitope which is recognized by cytotoxic T lymphocytes induced by an HIV protein or fragment or derivative thereof.

3. The method of Claim 2 wherein said protein or peptide or fragment or derivative thereof is an HIV protein or fragment or derivative thereof.

4. The method of Claim 1 wherein the mycobacteria are of the species M.bovis-BCG.

5. A composition for inducing a CTL response in an animal, comprising:

mycobacteria transformed with at least one DNA sequence which encodes a protein or peptide or fragment or derivative thereof which includes an epitope which is recognized by cytotoxic T lymphocytes, and an acceptable pharmaceutical carrier, said mycobacteria being present in an amount effective to induce a CTL response in an animal.

6. The composition of Claim 5 wherein said protein or peptide or fragment or derivative thereof includes an epitope which is recognized by cytotoxic T lymphocytes induced by an HIV protein or fragment or derivative thereof.

7. The composition of Claim 6 wherein said protein or peptide or fragment or derivative thereof is an HIV protein or fragment or derivative thereof.

8. The composition of Claim 5 wherein said mycobacteria are of the species M.bovis-BCG.

1147

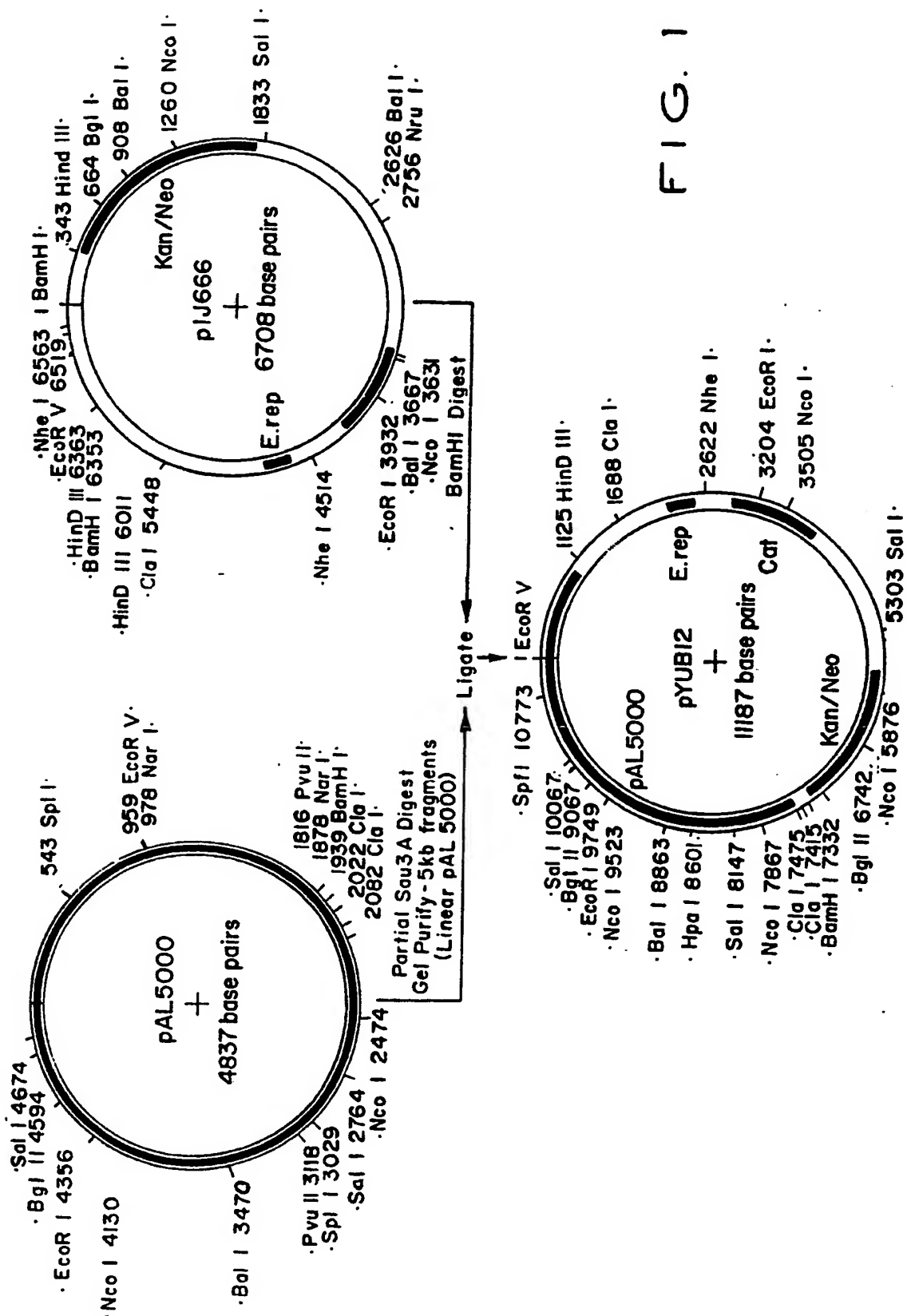


FIG. 1

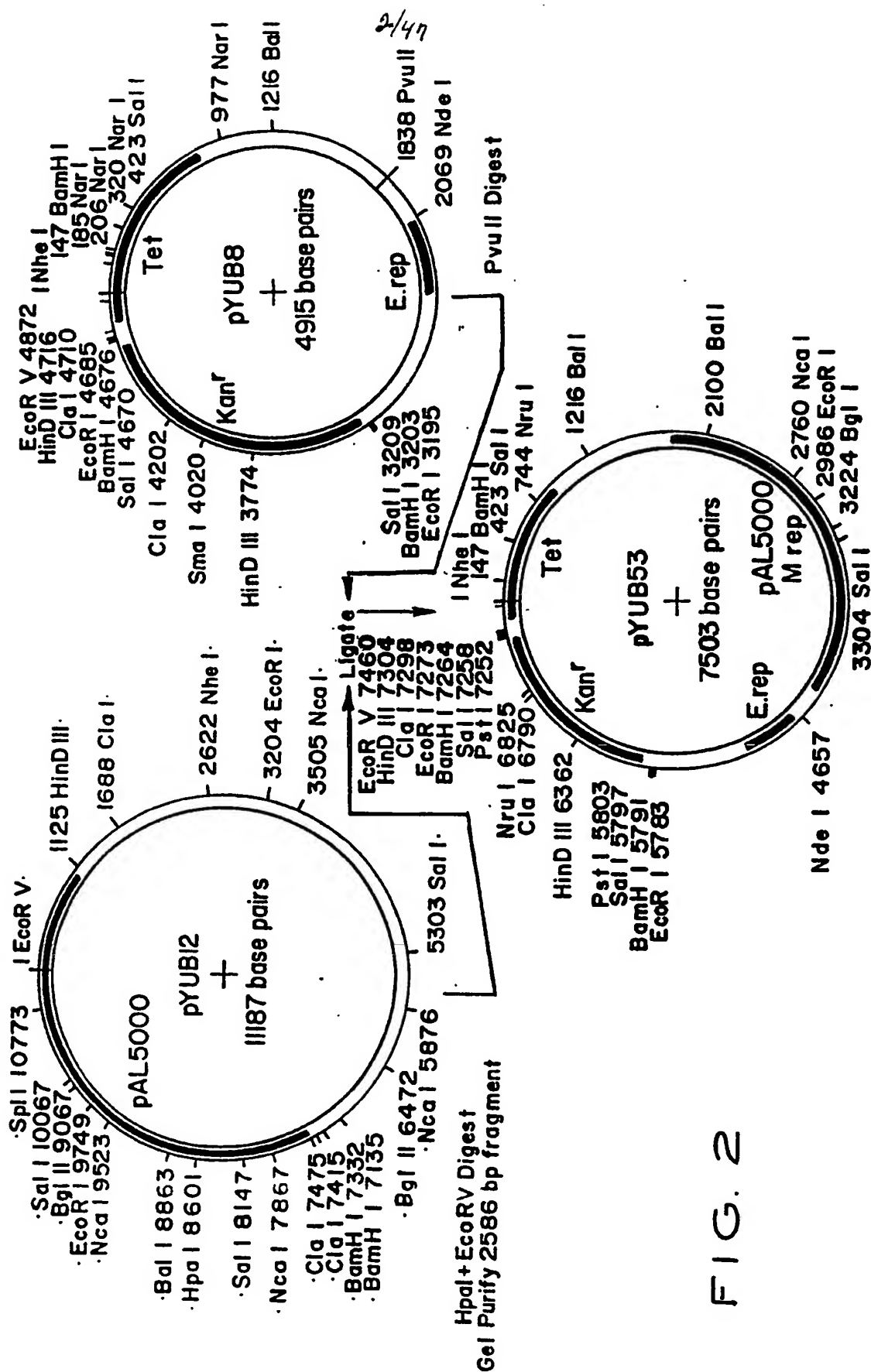


FIG. 2

FIG. 3

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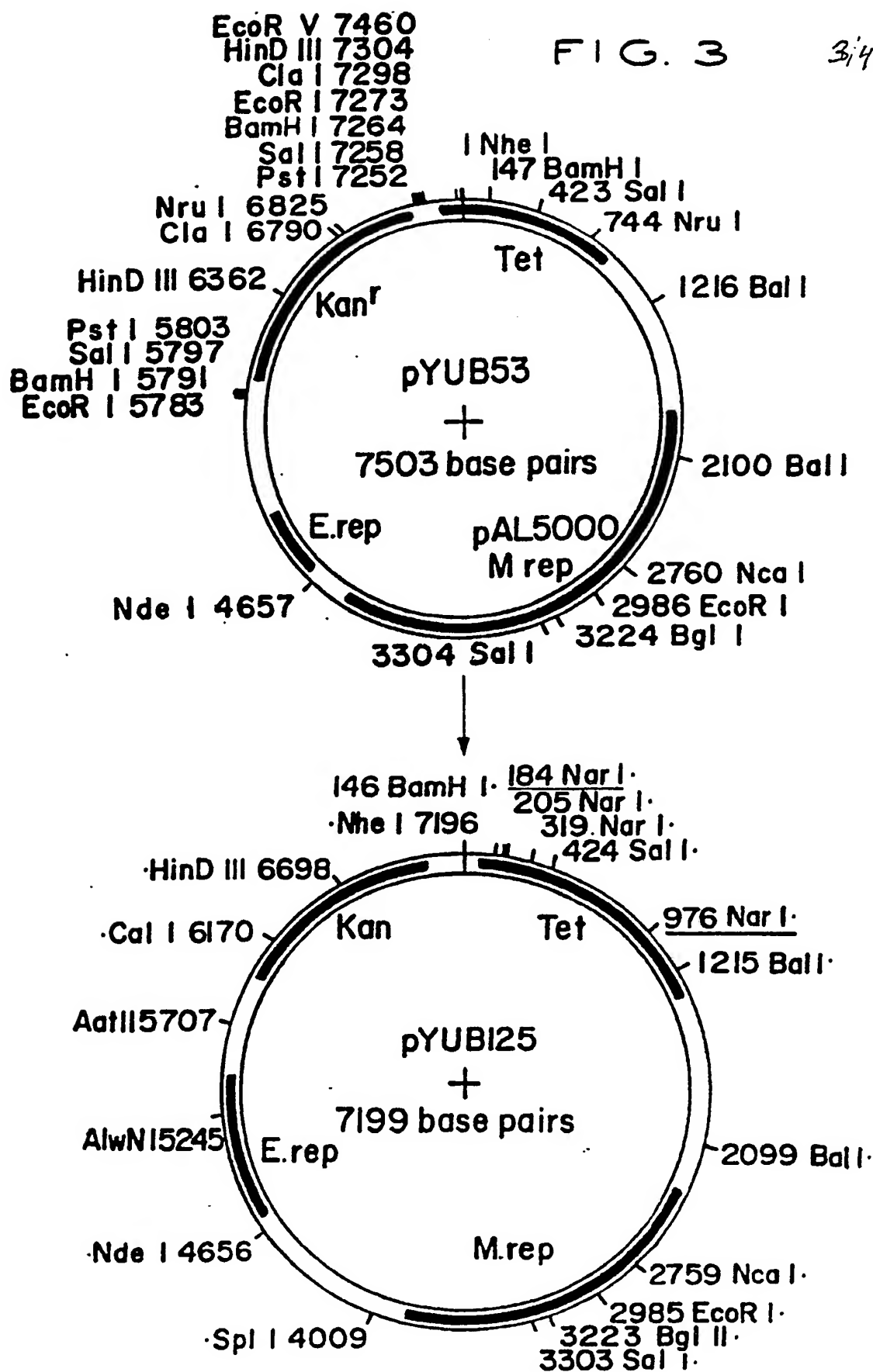
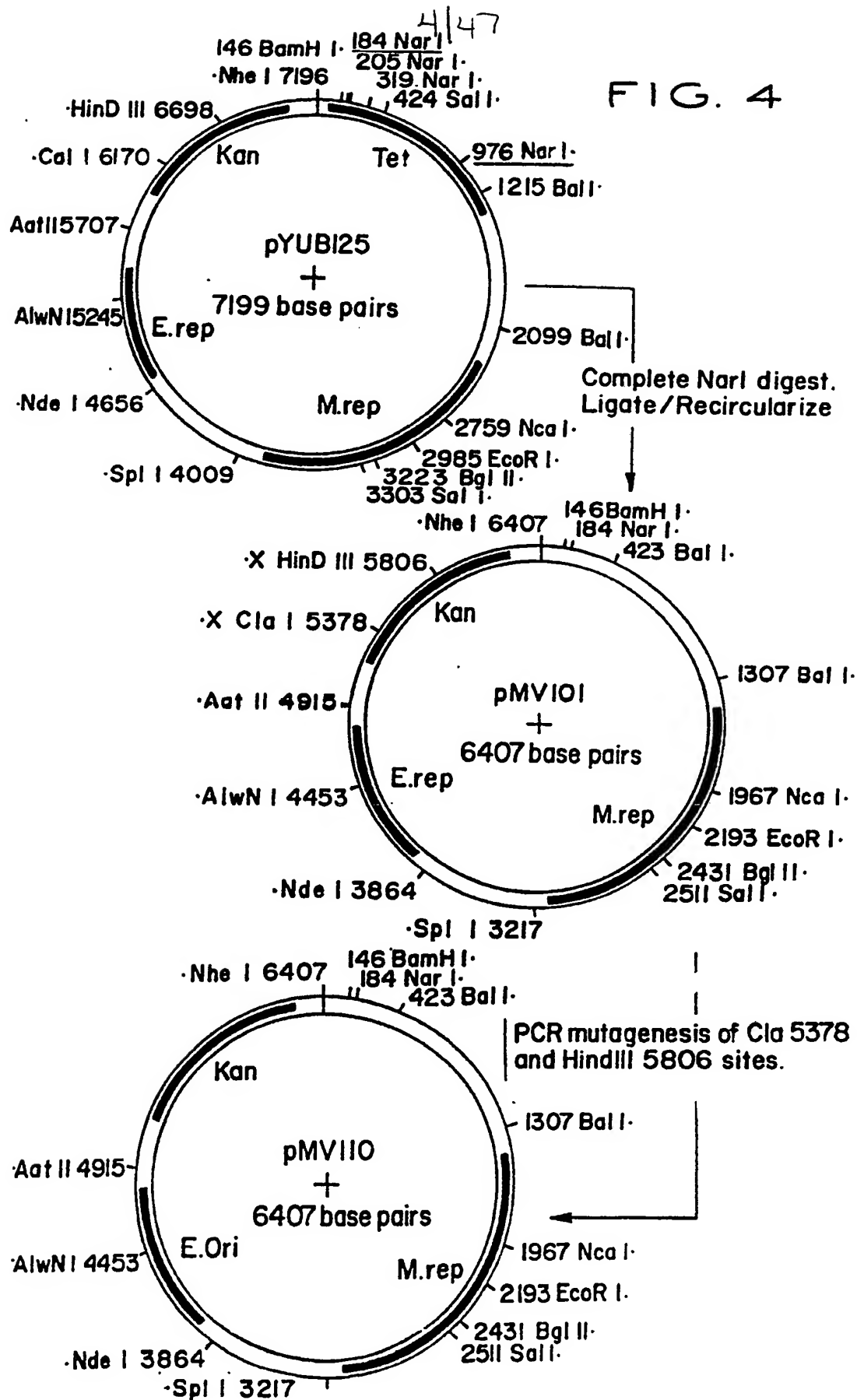


FIG. 4



SUBSTITUTE SHEET

5147
FIG. 5A

[illegible]

MATCH WITH FIG. 5B

SUBSTITUTE SHEET

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FIG. 5B

MATCH WITH FIG. 5A

ACTGTCCGAACCCCTTTGGCCGCGCCAGTCCCTGCTCGCTTCGCTACTT
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 100
GACAGGCTGGCGAAACCGGCGGGCGGGTCAGGACGAGCGAAGCGATGAA

→ N_{de}I

CTCTACCGGACGCGATCGTGGCCGGCATCACCGGCGCGCCCTATAAC
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 200
AGATGCCGCTGCGTAGCACCGGCGGTAGTGGCCGCGGGGGATATGG
CCTGAATGGAAGCCGCGGGCACTCGCTAAAGGATTCACTCACTCAAGA
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 300
CGACTTACCTTCGGCCCGCGTGGAGCGATTGCTTAAGTGGTGAGGTTCT
CGCATAACATATOCATCGCGTCCGCCATCTCCACCAAGCGCACGCGGC
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 400
CGTCTTGTATAGGTAGCGCAGGCGGTAGAGGTGCTCGGCGTGGCGCG

TCGTTGAGGACCGGCTAGGCTGGCGGGGTTCCTTACTCGTTAAGCA
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 500
ACACCAACTCCTGGGCCCATCCGAACGCCCAACGGAATGAACCAATCGT
GTCTGGACCTGAGCAACAACATGAATGGTCTTCCGTTTCCGTGTTTCG
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 600
AGACGCTGGACTCGTTGTGTACTTAACAGAAAGCCAAAGGCACAAAGC
GCATCGCAGGATGCTGCTGGCTAACCTGTGGAACACCTACATCTGTAT
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 700
CGTAGCTTCTTACCAACGACCGATGGGACCAATTGTGGATGTAGACATA
CCATAACGCCACTTGTTTACCTCACAACGTTCCAGTAACCGGGCATG
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 800
GGTATGGCGGTCAACAAATGGGAGTGTGTGCAAGGTCATTGGGCCGTAC
ATTACCCCATGAACAGAAATTCCTCCCTTACACGGAGGCATCAAGTGA
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 900
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.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1000
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GAGGACAGTCGACGACGAAGTTCTTCTGGATGCGCGCCGTGTGGGAAG
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1100
CTCCTGTCAGCGTGGTCTTCAAGAAGACCTAGCGCGGGCAACGACCTTC
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.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1200
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CGTTCGGTGAGCTGTCAACGGGGCCTGTAAACGGCACAACGAACCGTGCA
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1300
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TACATCACCACAACCAACGATTCTGGCGGTGAGCTCCACGATATTACCC
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1400
ATGTAGTCGTGTTGGTGTCTAAGACCGCCACTCGAGGTGCTATAAGTCC
GTATTCAAAACGGACGCAACGAAACACGCAACGAGACAGGCATGGCCC
.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1500
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```

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GAACAGCGGTGGATTGTCCGGCTTCGTTGTGGGCCCTTTTGAACCGCTTCCTG
1601-----+-----+-----+-----+-----+-----+-----+
CTTGTGCGCAOCTAACAGCCGAAGCAACACCCGAAAACTGGGCGAAGCAC
e F L P P N D A E N E A K Q A A E Q
TCCAGATGCAGCCCGAAATGTTTGCCCGTTTGCGGCCAAGAGTGGCCCTCGT
1701-----+-----+-----+-----+-----+-----+-----+
AGGTCTAOGTGGGCTTTACAAACCGGCAAAACGCGGTTCTCACCGGGAGCA
e L E L G F M K A T Q P W S E G E D
CCCAACTGCTGCGTTCTCGGCCAAGAGCCGGACGACGTGGCGTTTCGGAT
1801-----+-----+-----+-----+-----+-----+-----+
CGGTGAGCGAAGCAAGGACGCGGTGCTCGGCTGCTGCACCGCAAGCCTAT
e N E S R E Q A V L R V V H R E S L

GACAGTCCGGCTGCCGGTTGTAGCGTGTAGCCGTGCTGTAGCCGTGCTGTAGCCGTG
1901-----+-----+-----+-----+-----+-----+-----+
CTGTACGCGACCGCCCAACATCGGCAGCGACATCGGCAGCGACATCGGCAGC
d
e V T P C R W Y G D S Y G D S Y G D S
CTGTGCTGCGCGCGCTGCGCGCTGCTGCGGCCCTTCGCTAGATGGCCGACTG
2001-----+-----+-----+-----+-----+-----+-----+
CACACGACCGGGCGGCAACCGCGACCAAGCGCGAAGGGCGCTCTACCGGCTGAO
d I S A A T R A A A G K R S I A S Q
e H E G G W A S S R G E A L H G V P

GCGCGACTTGGTTGTGATCCAACGCCAAATGCTGTTGGCCATGGCCCCGAC
2101-----+-----+-----+-----+-----+-----+-----+
CGCGCTGAACCAACACTAGGTTGCGGTTTACGACAACCGCTACCGCGCGCTG
d R S X T T I W R W I S W A I A R V
e A V Q N E D L A L E Q Q R E R P G
GCGTTTCGCGCGTGGCACTCGGCATAGATCGCGCGGCGGAGTCCGTCCACG
2201-----+-----+-----+-----+-----+-----+-----+
CGCAAAGCGCGCACCGTGAGCCGTATCTAGCGCGCGGCTCAGGCAGGTG
d N R A R C E A Y I A R G L G D V
e R K A R P V R C L D R P R T R G R
ACCTGAACGAATCGAACAGTGGCAATTCCGCCCTAGCGGGGTGGAGCCG
2301-----+-----+-----+-----+-----+-----+-----+
TGGACTGCCTTAGCTTGTACGCGTTAAGGCGGGATCCCGCAGCCCTCGGC
d R V S D F L A C N R G L P T P A A
e Q R P R V T R L E A R A A D S G G

CAGCTCCGCTCGATGTGGCTGAGTGTGTAGAGATCTGAGTGGACCCATTCC
2401-----+-----+-----+-----+-----+-----+-----+
CTCGAGCCGGAGCTACACCGACTCACACATCTCTAGACTCACTCGGTAAAGG
d L E A E I E S L T Y L D E H L W E T
e A R G R E P Q T E L S R L P A M G
Sα,I,I C-T PCR MUTAGENOSISPHV110-300S
CTGCGGTGCGCGTGAAGCGCGCGGAAGGCCCTCGGGCGCACGCGCCATGT
2501-----+-----+-----+-----+-----+-----+-----+
GACGCCAGCGGCAGCTGCCGCGCGGCTTCGGAAGCGCGGTGCCCGGYAC
d R D G D V A R R I G E A C A A M T
e Q P R R R R R A S P R R R V

TGAGTCCCCACACTGCGTGTGCGTGGCGGTGGCGCGATTGCCACGATCGO
2601-----+-----+-----+-----+-----+-----+-----+
ACTCACGGGTGTGACGCACACGCAACCGGCAACCGCGCTAACGGGTGCTAGO
d L A W V A E A N G N A R N G V I A

```

MATCH WITH FIG. 5aB

FIG. 5aA

MATCH WITH FIG. 5aA

FIG. 5aB

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+.....+.....+.....+.....+ 1600
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+.....+.....+.....+.....+ 1700
 AAGACGGGCTGCGAGAAAGGAOCCCGCTATCGGCTCAGCGAATTGCCAC
 K A A R E K R A R Y G L R K V T D
 CGTCGTGATAGGCGGGATGCGTTCCGCGGCGTGCAOCCCTGCTCGGCCA
+.....+.....+.....+.....+ 1800
 GCAGCACTATCCGGGCTACGCAAGCGCCGACGTCGGACGAGCCGCT
 D E Y A R I R E R R A A Q E A L
 AGTCCGGTGATTCCGAGCGCTTCGGGCGGGTCAOCCGCGCTTTTTCGG
+.....+.....+.....+.....+ 1900
 CAGGCCACTAAGCTCGGGGAAGCCGCGCAGTCGCGCGGCGAAAAACCG
 G T I R A G E A A T V R R K K R
 M, c, q, I
 CTCATAGCAATGCTC CATGGCTGAOCCGGACTTTGCGGCGCGCGCAA
+.....+.....+.....+.....+ 2000
 GAATATCGTTACGGAGGTACCGACTGCGCCTGAAACGCGCGGCGGTT
 L L A S M A S A S K A R R A V
 M A T G G E S V R V K R A A C S
 GCGCGCACTGAGTGTGGCTGTAGACCACGATCCCGTCGCGCCAAAT
+.....+.....+.....+.....+ 2100
 CGOCCGTGACTCACAOCGGAGCATCTGGTGCTAGGGCAGGCGGGTTTA
 R A S L T A E Y V V I G D A W I
 A C Q T E G R L G R D R G G L E
 G-APCR MUTAGENOSIS
 ph VII0-300S IROcE
 CTCGCTGTCCGGTAGCGGTCCGGGACACAAGTCGTTGCACGG GAATTCC
+.....+.....+.....+.....+ 2200
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 R Q G T A T R S V R R Q V P I R
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 X R T P L Y I R M L A P R Y A W L
 E P D A P L D A E P R S S L G V V
 CTTTGTACTTGGTCTGCTCAOCCAGCGCGCGGTGGCATGTTCCGCC
+.....+.....+.....+.....+ 2400
 GAAACATGCACCAGACGACTGCGGTCCGCGCCGCCACCGTACAAGCGCGG
 K Y T T Q Q R W R P P P M W A G
 Q V E D A S A L A A T A H E R R
 GTTTCOCAGGCGATGTGGCCGGGTTTTTGGTTCATGAGGCCTGAGTAA
+.....+.....+.....+.....+ 2500
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 E W A I H G P M K T M L G S Y S
 N G L R W P R P K Q D E P R L L
 ATGCGAGGGCTTAOCCGCGGTATTGGTGGTGGAACAGGGGCGT
+.....+.....+.....+.....+ 2600
 ATACGCTOCCGAATGCGGCGGCATAAGCCACGCACCTTGTCCCGCA
 A L P K R R A Y E T R P V P A N
 GTTGGGCAGCGATGGGAOCCCGGGGCTGAGCGCTCGGAGCGCTGC
+.....+.....+.....+.....+ 2700
 GCAACCCGTCCCTAACCTGGGGGCGGCGACTGCGAGCGCTCGGAGC
 N P L P N S G R A S L A R L A A

SUBSTITUTE SHEET

FIG. 5

[illegible]**COGNATE**

6401-----6407

CCCAOCHA

MAB-SPE

SUBSTITUTE SHEET

74/11

IISP 61 Cassette

[illegible]

60

13147
FIG. 7

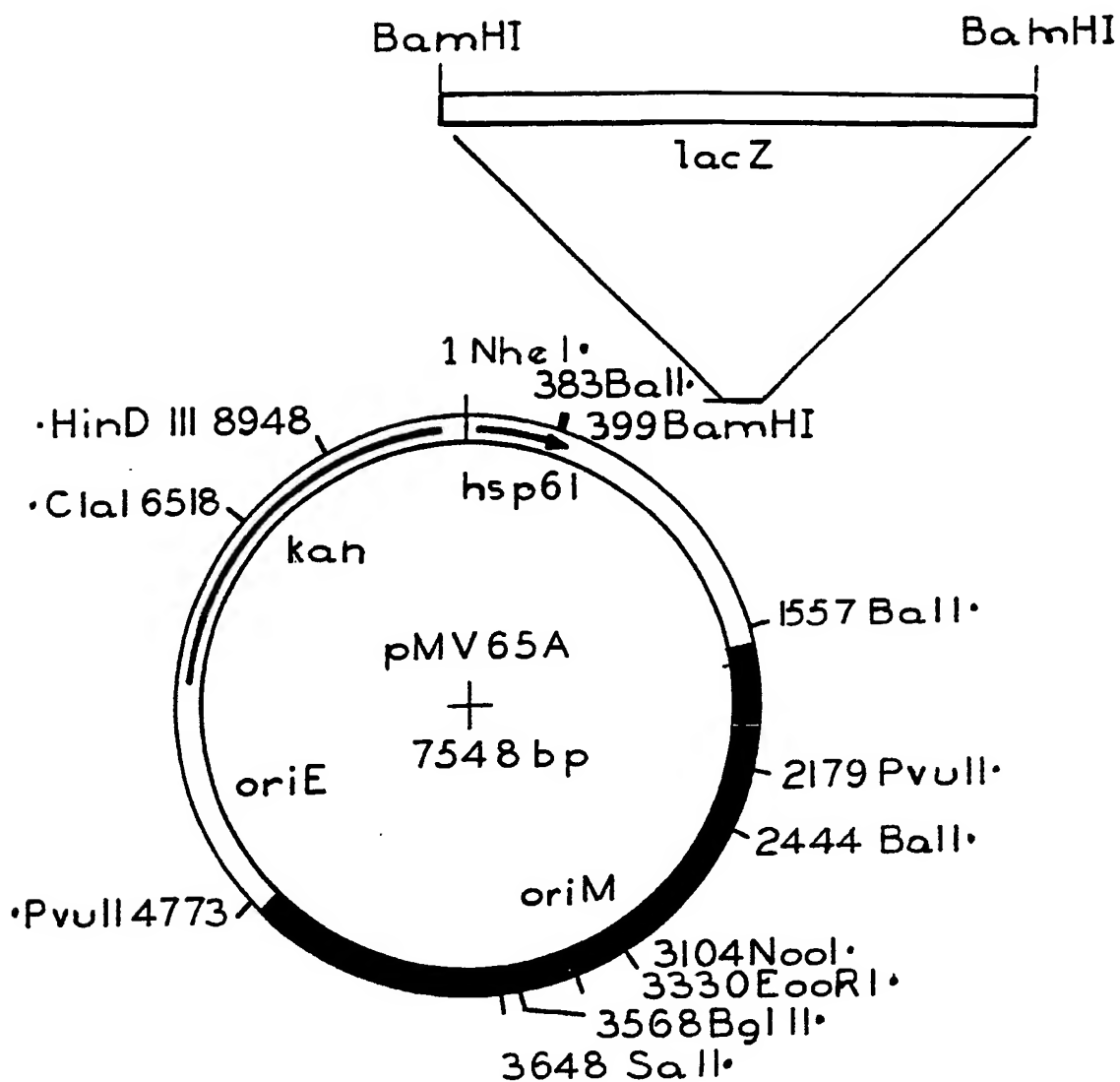


FIG. 8

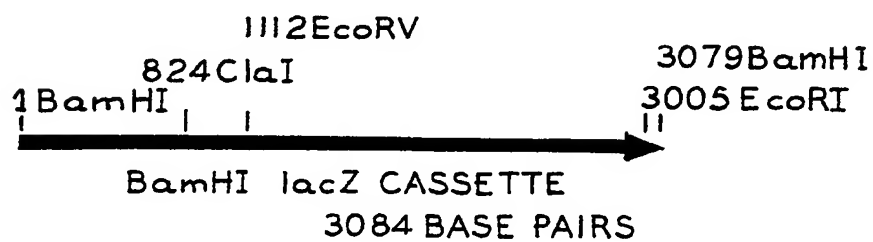
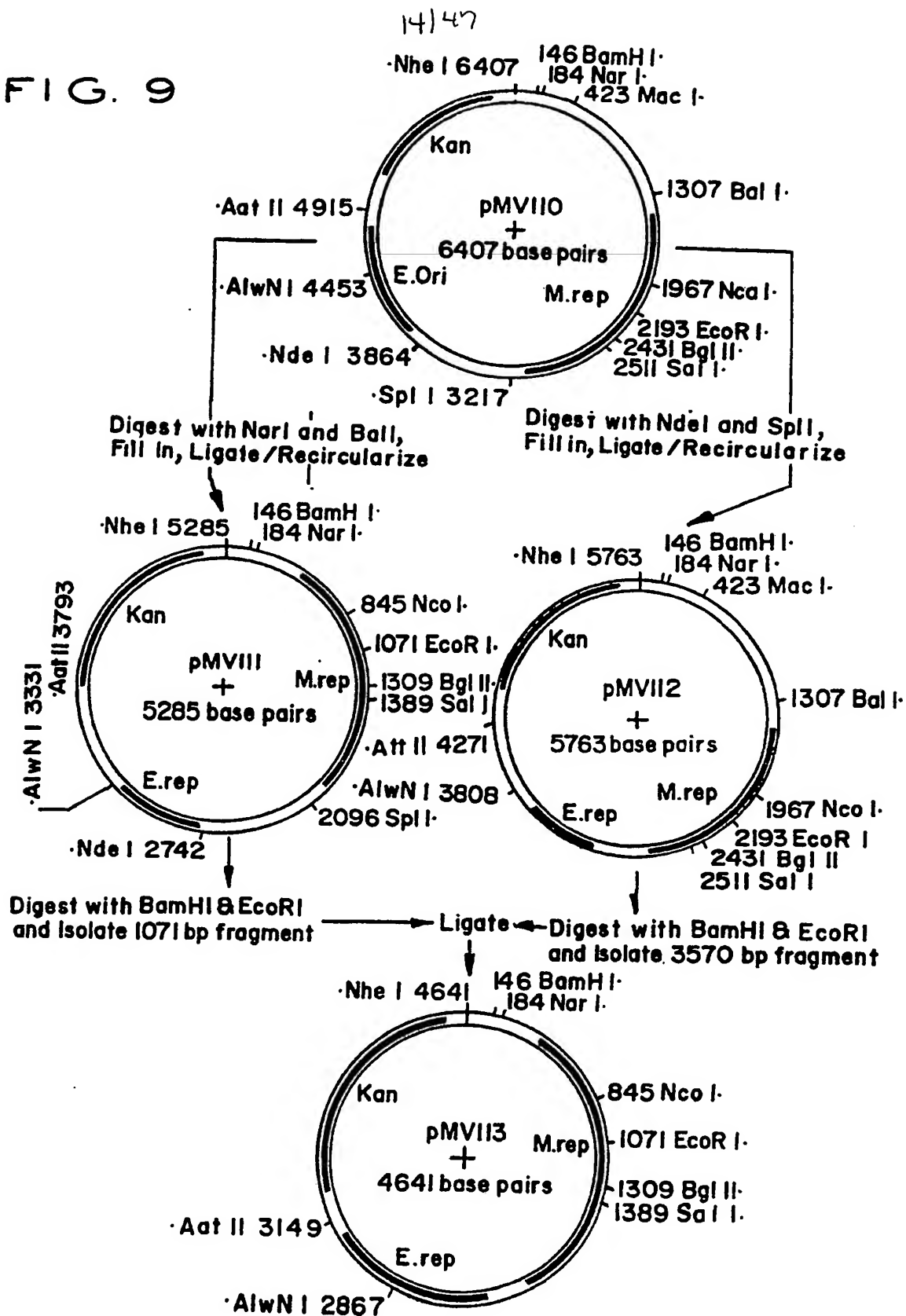
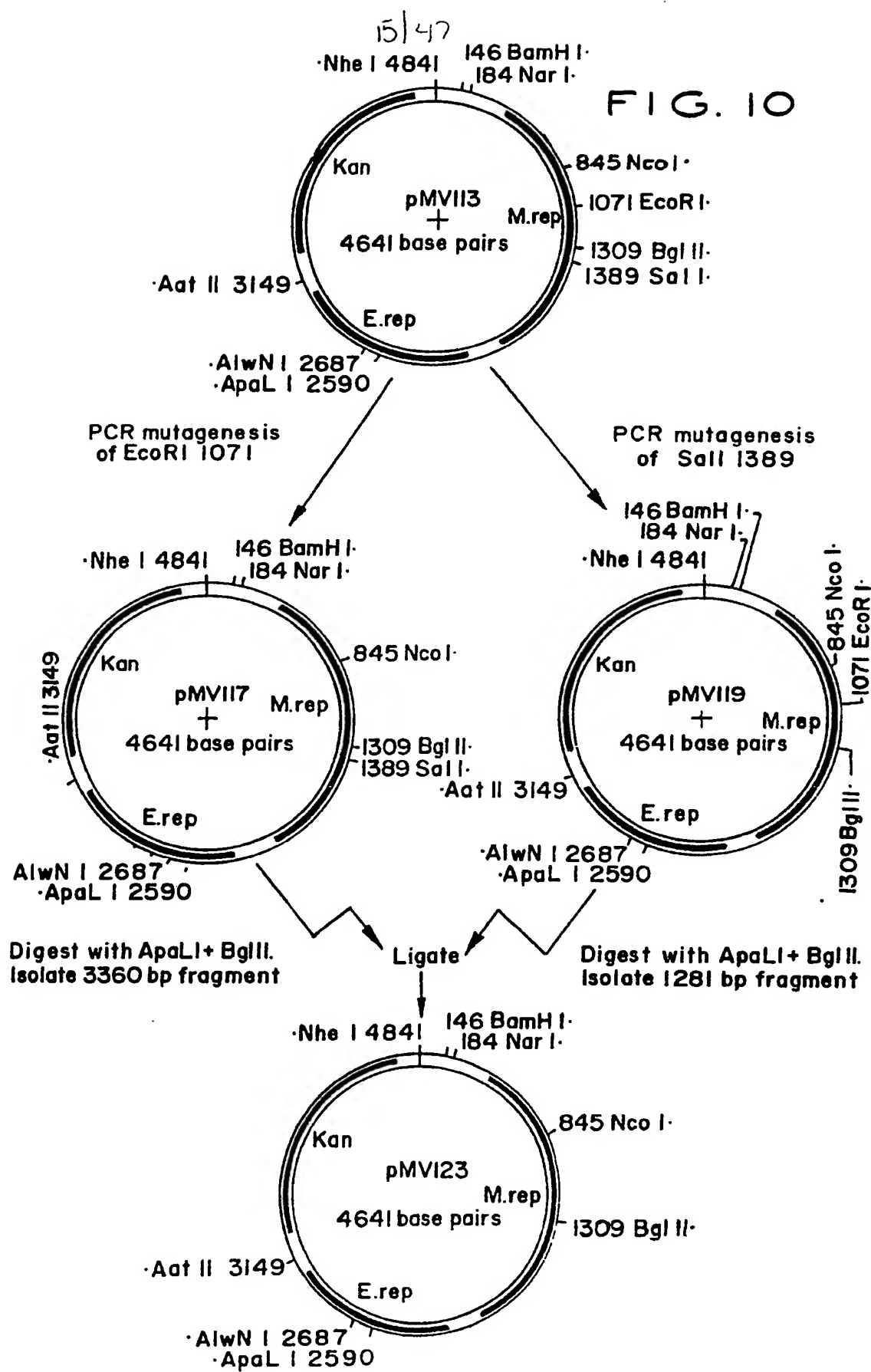
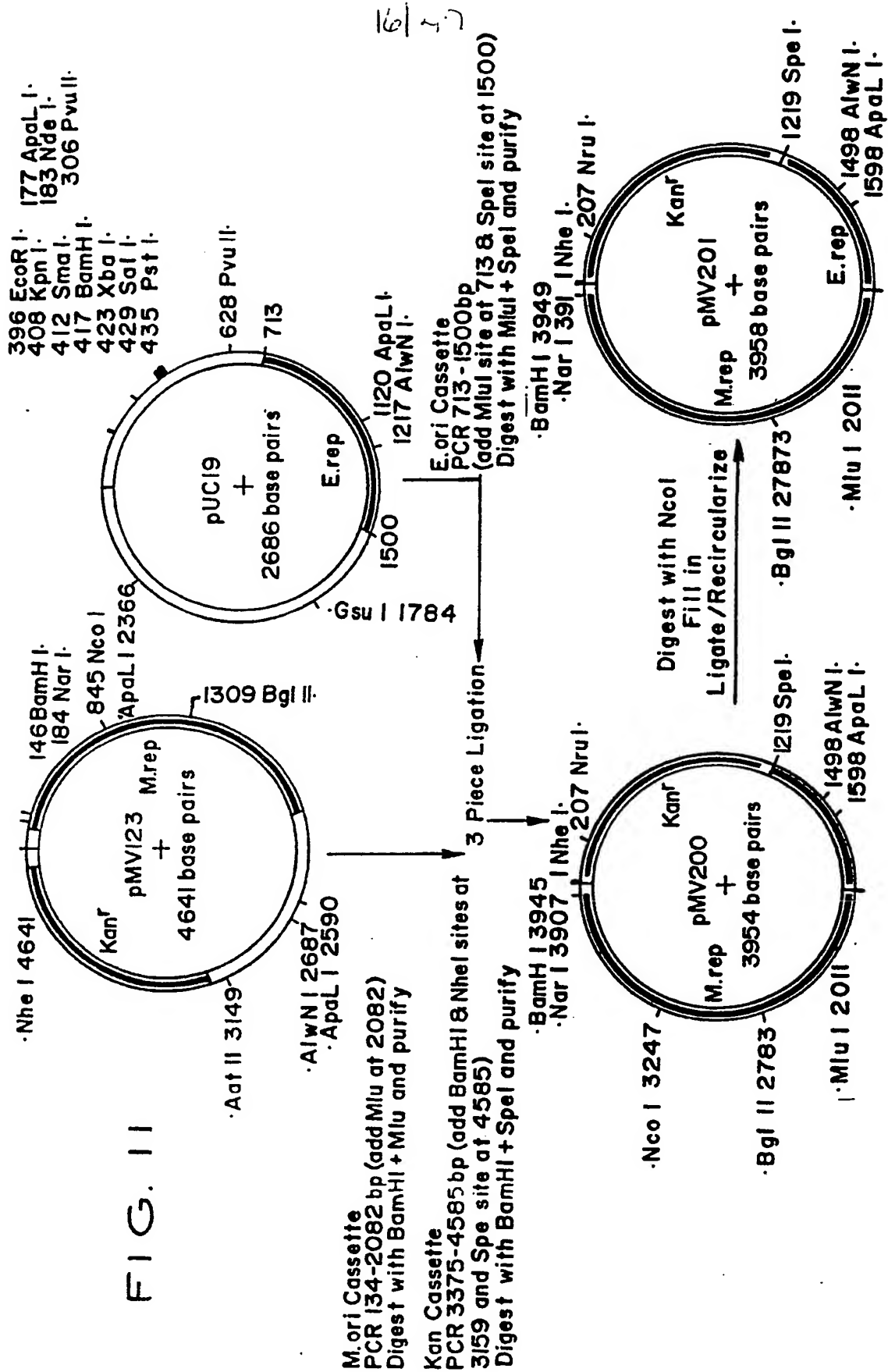


FIG. 9





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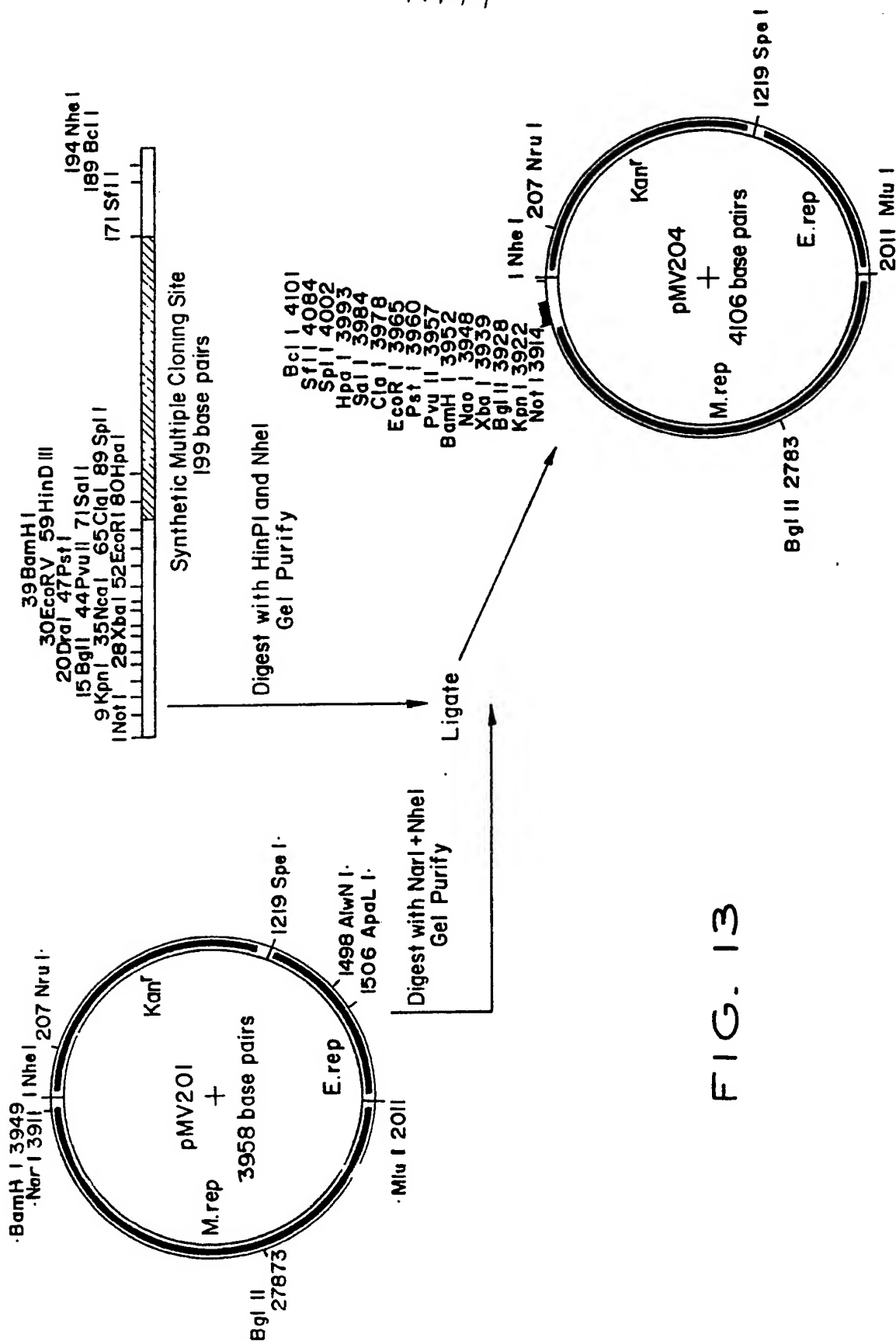
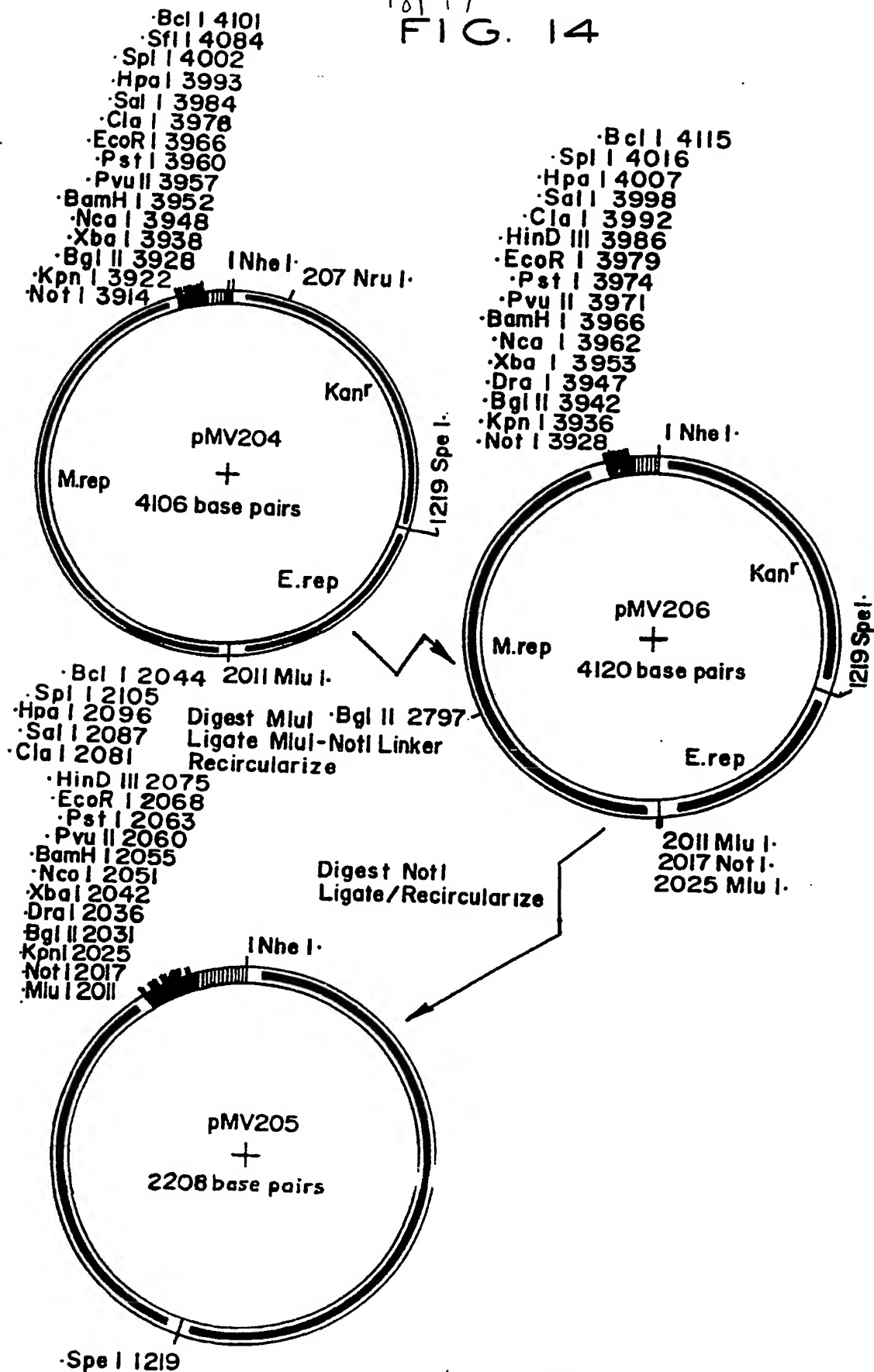


FIG. 13

18147
FIG. 14

SUBSTITUTE SHEET

19 | 47

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 1601-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 1701-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 1801-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 1901-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 END E.rep I,U,I,M I,t,a,N I,U,I,M BEGIN M.rep
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 2001-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2101-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2201-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2301-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2401-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2501-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 2601-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 AGGCCTTCGGCGCGCGGTGGAAGGAGACCGCAGTTACTCAGGCCTTATGA
 2701-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 CTCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCI
 2801-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 GGCGGAATTGGCACTGTTTCATTCCGTACAGGTGTGGGCCTATCGTCCCG
 2901-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
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 CGCGATCTATGCCGAGTGCACCGCGCGAAACGGCGAATTTCCGTGCAACG
 3001-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
 GCGCTAGATACGGCTCACGGTTCGGCGCTTTCGGGCTTAAAGGCACGTTC
 AGCATTTCGGGTGGATCACAACCAAGTCGGCGCATTTGGGCGGACGGGAT
 3101-.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+
 TCGTAAACCGCAACCTAGTGTGGTTACGCGCGTAAACCGCGCTGCCCTAG

MATCH WITH FIG. 15aB

FIG. 15aA

SUBSTITUTE SHEET

MATCH WITH FIG. 15a.A

FIG. 15a.B

20 | 47

GATAGTTAOCGGATAAGGCCGACGGCTCGGGCTGAAOCCGGGGTTCGTG
 -----+-----+-----+-----+-----+ 1600
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 GCGTGAGCATTGAGAAAGCCGACGCTTCCCGAAGGGAGAAAGCGCGAC
 -----+-----+-----+-----+-----+ 1700
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 TCCAGGGGGAAACGCTGATCTTTATAGTCTGTGGGGTTTCGCCACC
 -----+-----+-----+-----+-----+ 1800
 GGTCCCCCTTTCGGGACCATAGAAATATCAGGACAGCCAAAGGGTGG
 TGGAAAAACGCCAGCAACCGCGCCTTTTTACGTTCCTGGCCTTTTGCTG
 -----+-----+-----+-----+-----+ 1900
 CCTTTTTCGGGTGTTTCGGCCGAAAAATGCAAGGACCGGAAAAACGAC
 CCGTATTACCGCCTTGAGTGAAGCTGATACCGCTCGCCGACCCGAACG
 -----+-----+-----+-----+-----+ 2000
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TCGGGCGCTGTGTGGCTGTACCCGCGCATTACAGGCGGCAGGGGGTCTA
 -----+-----+-----+-----+-----+ 2100
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 GAAACGTCTTCGAAACGACGCATGTGTTCTCTCTGGTTGGTACAGGTGGT
 -----+-----+-----+-----+-----+ 2200
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 AGCGGGGGAGTGTGCAAGTTGTGGGGTGGCCCCCTCAGCGAAATATCTGACT
 -----+-----+-----+-----+-----+ 2300
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 -----+-----+-----+-----+-----+ 2400
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 -----+-----+-----+-----+-----+ 2600
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 -----+-----+-----+-----+-----+ 2700
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 -----+-----+-----+-----+-----+ 2800
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 -----+-----+-----+-----+-----+ 2900
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 -----+-----+-----+-----+-----+ 3000
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 ACGTGTGTCCCGGACCGCTACCGGACAGCGAGGTCCGCGCCATCGCCAAC
 -----+-----+-----+-----+-----+ 3100
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 -----+-----+-----+-----+-----+ 3200
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SUBSTITUTE SHEET

21/47

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 ATCCCTCGAGCAGATOGTGGCTTGCCAGCGCCAGTACGGCAGCCA
 2801-.....+.....+.....+.....+.....+
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 d G E L L D D S A L P W Y P L W
 TAATCACC GG TGTATGGTCCGACACGACCTOCAAGTCAGATATTTCC
 2901-.....+.....+.....+.....+.....+
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 T V P T N D S V L E L D S I E S
 TGATGAAACAACCAACCCACAGCCGAGCACCCCAACCACCTGTACCAAC
 3001-.....+.....+.....+.....+.....+
 ACTACTTTGTGGTTCGCTGTGGCTCGTCCGCGTTGGTGGACATGGTTG
 d S S V G A V A S C G W G G T G
 CTGTCCCGCCCGTACACGCGCCCTAGAACCGTTAGACCCCTGCGCG
 3101-.....+.....+.....+.....+.....+
 GAGACCGCGGCATGTGGCGGGAATCTGGGGAATCTGGGGGACCGG
 S, P, L, I]
 CTCACCTGGCTTTATGGCGTAOGAATCGGCTGTGTGGACCTGTGGGO
 3201-.....+.....+.....+.....+.....+
 CAGTGGACCGAAATACCGCATGCTTAGCCGACACACGCTGGACAACCCG
 CGAGCCCGCAACGGCCGCGCGCGGTGTCAACAACCGGGTGAGTGTGCAC
 3301-.....+.....+.....+.....+.....+
 GCTCGGGGCTGCGCGCGCGCGCCACAGTTGTGTGGCCACTCAGCACGTG
 CCGCCCGATGAGCCGCGCTTACGCTGGCTGOCAGCCGTTCCGGGCTCG
 3401-.....+.....+.....+.....+.....+
 GCGGGGCTACTCGGCGGGAATGCGACCGACGGTCCGCAAGCGCCGAC
 AGGCTCGCCCTTTTAAGGCTGAATTTGCTTGTCTCCGAATCCAAGTGG
 3501-.....+.....+.....+.....+.....+
 TCCGGAGCGGGAATAATCCGACTTAAACGAACAGAGGCTTAGGTTGAC
 ACACATGACCAACTTCGATAACGTTCTCGGCTGATCTCCCTCGCGGTT
 3601-.....+.....+.....+.....+.....+
 TGTGTACTGGTTGAAGCTATTGCAAGAGCCGAGCTAGACGGAGCCCGCA
 ACAGCTTGTCTGTAAGCGGATGCGCGAGCAGACAAGCCGTCAGGGCGO
 3701-.....+.....+.....+.....+.....+
 TGTGGAACACACATTCCCTACGGCCCTCGCTGTTCGGGCAGTCCCGCG

 GCGATAGCCGACTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGT
 3801-.....+.....+.....+.....+.....+
 CGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCTAACA
 AGAAAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTG
 3901-.....+.....+.....+.....+.....+
 TCTTTTATGGCGTAGTCCGCGAGAACCGAAGGAGCGAGTGACTGAGCGAC
 TAATACGGTTATCCACAGAATCAGCGGATAACGCAGGAAAGAACATCTGAG
 4001-.....+.....+.....+.....+.....+
 ATTATGCCAATAGGTCTCTTAGTCCCTATTGCGTCTTTCTTGTACACTC
 GTTTTTCATAGGCTCCGCCCGCGTACGAGCATCAAAAAATCGACGCTC
 4101-.....+.....+.....+.....+.....+
 CAAAAAGGTATCCGAGCCCCGGGACTGCTCGTACTGTTTTTACCTCCGA
 CCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTGCGGCTTAC
 4201-.....+.....+.....+.....+.....+
 GGCGACCTTCGAGGGAGCACCGGAGAGGACAAGGCTGGGACGGCGAATG

MATCH WITH FIG. 15bB

FIG. 15bA

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5GTTCCTCGATGTAACGGCGCCCTAGGGCCGACGCGCGGCTTTGGCGTAG
 +-----+-----+-----+-----+-----+-----+
 CAACCCAGCTACATGGCCGCCGATCCCGCTGCGCGCGAAGCCCATC 2800
 M A E I Y R R G L A S A R S Q R Y I
 3AGCTGCTCAAATTOGTGCGCGAOGTGGCTCAOGCTTGTTAGTAGACCAAGAT
 +-----+-----+-----+-----+-----+-----+
 CTGACGAGTTTAAGCAGCCGCTGCAACGAGTGGGAAACATCATCTGGTGCTA 2900
 L Q E F E D A V M S V S P L L G R N
 TGAGGGGGCCACCCACAACTGCACACTCCCGCTCTCCCGTCGAGCCCTGA
 +-----+-----+-----+-----+-----+-----+
 ACTCCCGGTTCCGGTGTGTGACGTGTGAGGGGGCGAGAGGGCAGCTCGGGACT 3000
 L P W G V V A C E G A R G D L G S
 CAGGAGGAACACATGCGTGTGTTGAGGGAOGTTTCCGGGCGCTAAGAGCCG
 +-----+-----+-----+-----+-----+-----+
 GTCTCTCTTGTGTACGCAGCAAGCTCCTGCAAAGGCCCGGCGATTCTGGGC 3100
 V L L F V
 CTGAATCCGCGGTTACGAGCCACACAGCACCCGAACCTTACGGAGCTGGTGGG
 +-----+-----+-----+-----+-----+-----+
 GGACTTACGCGCCATGCTCGGTGTGTCTGGGGCTTGATGCTCGACCAACC 3200

M. rep - Mlu

[illegible]

I, C, d, M

[illegible]

MATCH WITH FIG. 15bA

15.10.15

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AGGGCGCAGCAGCGCGCACGGCGGCGAGCACAGTTGCGGGGGGCGCAAAG
 3201-+-----+-----+-----+-----+-----+-----+
 TCCCGCGTGGTGGCGCGTGGCGCGCTGGTGTCAAAGCGCGCGCGCGTTTCA

CGGCTACAGCGACGGCTACAACGGGCAGCGACTGTCCGCAAAAAGCGGGG
 3301-+-----+-----+-----+-----+-----+-----+
 GCGATGTGCGCTGCCGATGTTGGCGTGGCTGACAGGGGTTTTTGGCGCG

GTCGTCCGGCTGGTGGCGCAGGAAAGCAGCGAGTGGCTCGCGAGCAGGC
 3401-+-----+-----+-----+-----+-----+-----+
 CAGCAGGCGAGCAACCGCGTCTTGGCTGCTCACCAGCGGCTCGTCCG

GGCGCAAAAGGCCAAACATTTCCGGGCTGCATCTGGACACCGTTAAGCGA
 3501-+-----+-----+-----+-----+-----+-----+
 CCGGCGTTTGCCGGTTTGTAAAGCCGACGTAGACCTGTGGCAATTCGCT

AAAGGCCACAAAGAGCGGACAATCCAACCGCTGTTCTAAAGCAATTGG
 3601-+-----+-----+-----+-----+-----+-----+
 TTTCGGGTGTTGCTTCGGCTGTTAGGTGGCGACAAGATTGCGTTAAC

CAGGTAAAAGTCCTGGTAGACGCTAGTTTTCTGGTTTGGGCCATGCCT
 3701-+-----+-----+-----+-----+-----+-----+
 GTCCATTTTCAGGACCATCTGCGATCAAAAAGACCAAAACCGGTACCGA

GGGTTCTAOGAATCTTGGTCGATACCAAGOCATTTCCGCTGAATATCG
 3801-+-----+-----+-----+-----+-----+-----+
 COCAAGATGCTTAGAACCAGCTATGGTTCGGTAAAGGCGACTTATAGC

MATCH WITH FIG. 15c B

Multiple Cloning Site

		S	B
	N	K	g
End M. rep	o	c	p l
	t	I	n I
	I	I	I I

TTGTAGTGTGTGGTGGCATCCGTGGCGCGGCGCGGTACCAGATCTT
 3901-+-----+-----+-----+-----+-----+-----+
 AACATCACAAACACCGTAGGCACCGCGCGGCGCATGGTCTAGAA

	S	
Stop Condons	p	Begin Transcription Terminator
3 Frames	I	
	I	

GACGTAGTTAACTAGCGTACGATCGATCGOCAGGCATCAAATAAAACG
 4001-+-----+-----+-----+-----+-----+-----+
 CTGCATCAATTGATCGCATGCTAGCTGACGGTCCGTAGTTTATTTTGT

	S	
S	a	B
f	c	c
I	I	I
I	I	I

CATCATGGCCGCGGTGATCA
 4101-+-----+-----+-----+-----+-----+-----+
 GTAGTAACGGGCGCCACTAGT

FIG. 15c A

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FIG. 15cB

MATCH WITH FIG. 15cA

TCCGCGTCAGOCATGCATGGAGGCATTGCTATGAGCGACGGCTACAGCGA
.....+.....+.....+.....+.....+ 3300
GGCGCAGTCGGTTACGTACCTCOGTAACGATACTCGCTGCGCATGTGCT

CGTGACCGCGCGGAAGGCGCTCGAATCAOCCGACTATCOGAACGCCAC
.....+.....+.....+.....+.....+ 3400
GCACTGGGGCGGCTTCCGCGAGCTTAGTGGCCTGATAGGCTTGCGGTG

TGCAOCCGCGAAOCCATCCGCGCCTATCAOGAOAGAGGGGOCATCTT
.....+.....+.....+.....+.....+ 3500
ACGTGCGGCGCTTGCGTAGGCGCGGATAGTGCTGCTGCCGCTGAGAA

CTCGGCTATCGGGCGAGGAAAAGAGCGTGCGGCAGAACAGGAAGCGGCTCA
.....+.....+.....+.....+.....+ 3600
GAGCOGATAGCCCGCTCCTTTCTCGCAOCCGCTCTTGCTCTGCGGAGT
GGAGCGGGTGTGCGGGGGTTCCGTGGGGGGTTCCGTTCGAACGGGTGGGA
.....+.....+.....+.....+.....+ 3700
CCCTCGCCACAGCGCCCCCAAGGCAACCCCAAGGCAACGTTGCCCAGCCT

GTCTCGTTGCGTGTTTCGTTGCGCCCGTTTTGAATACCAGCCAGACGAGACG
.....+.....+.....+.....+.....+ 3800
CAGAGCAACGCACAAAGCAAOCGGGCAAACTTATGGTCCGCTCTGCTCTGC

GGGAGCTCACCGCCAGAATCCGTTGGTTGTGGTGATGTACGTGGCGAACTCCG
.....+.....+.....+.....+.....+ 3900
CCCTCGAGTGCGCGTCTTAGCCACCAACACCACTACATGCACCGCTTGAGGC

						H		
						I		
						n		
D	X	E	B	P	E	d	C	S
r	b	c	N	v	Pc	I	I	
		o	c	u	so	I		
		R	o	I	tR	I		I
I	I	V	I	I	II	I	I	I

TAAATCTAGATATCCATGGATCCAGCTGCAGAATTCGAAGCTTATCGATGTC
.....+.....+.....+.....+.....+ 4000
ATTTAGATCTATAGGTACCTAGGTGACGTCTTAAGCTTCGAATAGCTACAG

AAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTGTCCGGC
.....+.....+.....+.....+.....+ 4100
TTCCGAGTCAGCTTTCTGACCCGGAAGCAAAATAGACAACAAACAGGCCG

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FIG. 15B

90

MATCH WITH FIG. 15A

AAGATAAAATATATCATCATGAACAATAAACTGTCTGCTTACATAA
+.....+.....+.....+.....+ 100
 TTCTATTTTATATAGTAGTACTTGTATTTTGACAGACGAATGTATT

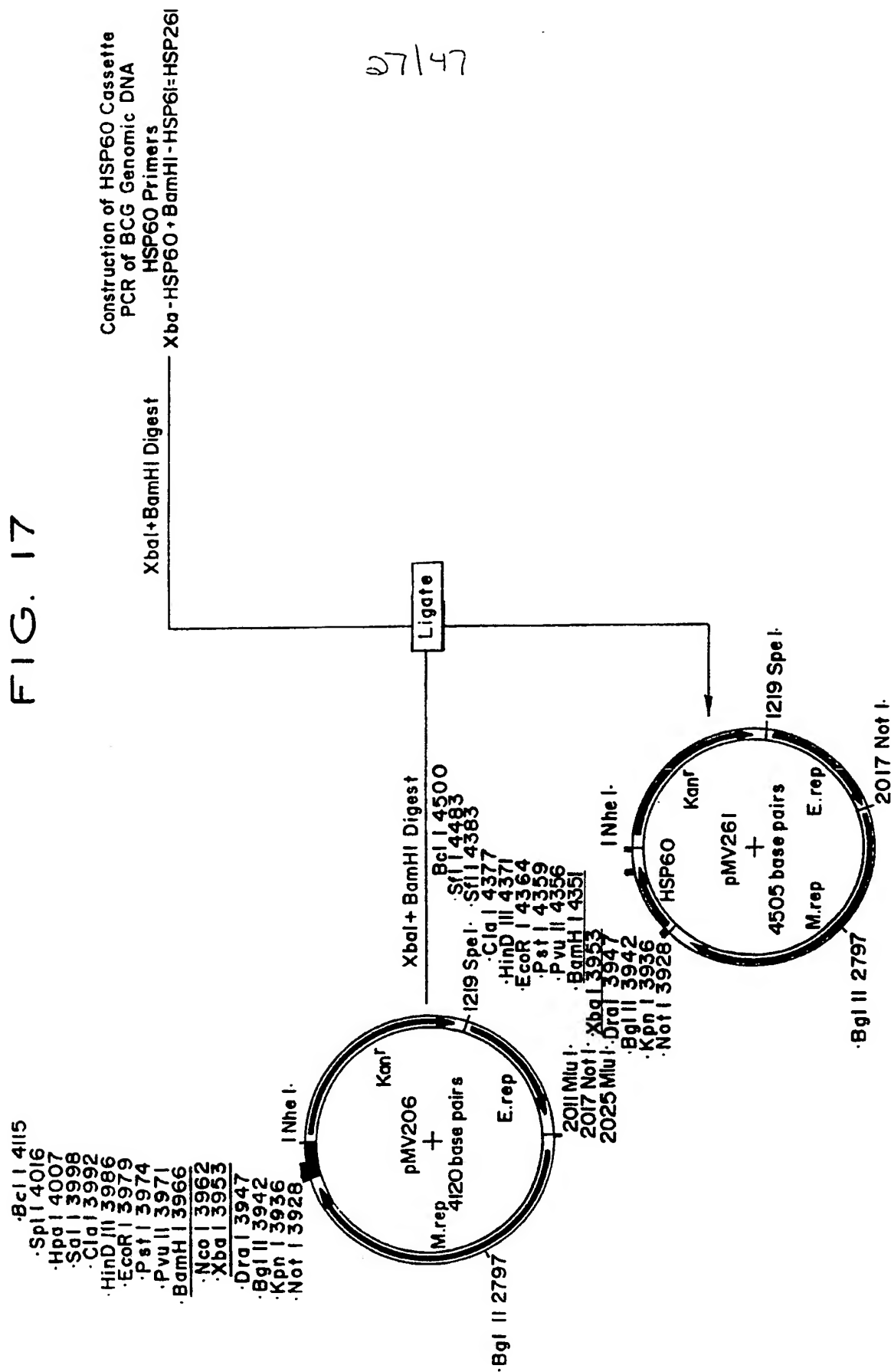
 GAGGCGCGGATTAAATTCCAACATGGATGCTGATTTATATGGGTATAA
+.....+.....+.....+.....+ 200
 CTCCGGGCGCTAATTTAAGGTGTACCTACGACTAAATATACCCATATT
 GGGGAAGCCCCATGCGCCAGAGTTGTTTCTGAAACATGGCAAAGGTAGC
+.....+.....+.....+.....+ 300
 ACCCTTCGGGGTACGCGGTCTCAACAAAGACTTTGTACOGTTTCCATCG
 TTTATGCCTCTTCCGACCATCAAGCATTTTATCOGTACTOCTGATGATG
+.....+.....+.....+.....+ 400
 ATACGGAGAAGGCTGGTAGTTCGTAATAATAGGCATGAAGGACTACTAC
 AGAATATCCTGATTGAGGTGAAAATATTGTTGATGCGCTGGCAGTGT
+.....+.....+.....+.....+ 500
 TCTTATAGGACTAAGTCCACTTTTATAACAACCTACGCGACCGTCACAA
 GCGTATTTGCTCTCGCTCAGGCGCAATCAGGAATGAATAACGGTTTG
+.....+.....+.....+.....+ 600
 GCGCATAAAGCAGAGCGAGTCCGCGTTAGTGCTTACTTATTGCCAAAC
 TCTGGAAGAAATGCATAATCTTTTGCCATTCTCAACGGATTGAGTGC
+.....+.....+.....+.....+ 700
 GACCCCTTCTTTACGTATTAGAAAAACGGTAAGAGTGGCCTAAGTCAGC
 ATAGGTTGTATTGATGTTGGACGAGTCGGAATCGCAGAACCGATACCA
+.....+.....+.....+.....+ 800
 TTATCCAACATAACTACAACCTGCTCAGCCTTAGCGTCTGGCTATGGT
 GAAACGGCTTTTTCAAAAATATGGTATTGATAATCCTGATATGAATAAA
+.....+.....+.....+.....+ 900
 TCTTTGCCGAAAAAGTTTTTATACCATAACTATTAGGACTATACTTATT

 GGTGTGAACACTGGCAGAGCATTACGCTGACTTGACGGGACGGCGGCT
+.....+.....+.....+.....+ 1000
 CCAACATTGTGACCGTCTCGTAATGCGACTGAACTGCCCTGCCGCCGA
 CCGACAACGCAGACCGTTCOGTGGCAAAGCAAAAGTTCAAAATCACC
+.....+.....+.....+.....+ 1100
 GGCTGTTCGCTCTGGCAAGGCACCGTTTCGTTTTCAAGTTTTAGTGG
 GCTGGATGATGGGGCGATTGAGGCTGGTATGAGTCAGCAACACCTT
+.....+.....+.....+.....+ 1200
 CCGACCTACTACCCCGCTAAGTCGGGACCATACTCAGTCGTTGTGGAA

 GATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTG
+.....+.....+.....+.....+ 1300
 CTAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGAC
 GAGCTACCAACTCTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAG
+.....+.....+.....+.....+ 1400
 CTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCGCGTC
 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAG
+.....+.....+.....+.....+ 1500
 TGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTC

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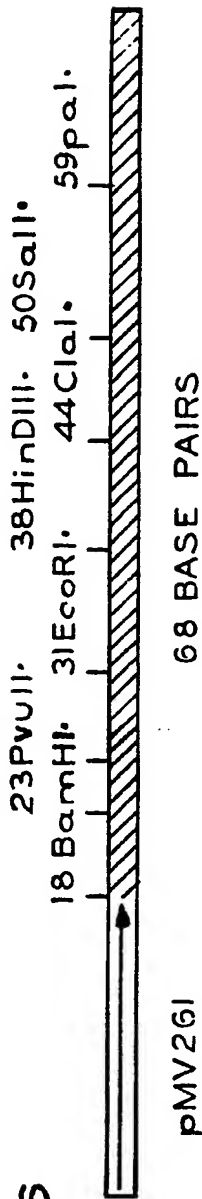
FIG. 17



ATG GCC AAG ACA ATT GCG GAT CCA GCT GCA GAA TTC GAA GCT TAT CGA TGT CGA CGT AGT TAA CTA GC

25 PstI.

FIG. 16



READING FRAMES AND RESTRICTION SITES IN MCS OF pMV261
 THE HSP60 GENE SEQUENCE STARTS AT THE ATG START CODON OR BASE 4334 OF pMV261 AND ENDS AT THE UNDERLINED BamHI SITE. THE SYNTHETIC MCS BEGINS AT THE BamHI SITE. THE DIRECTION OF HSP60 TRANSCRIPTION AND TRANSLATION IS INDICATED BY ARROW. SYNTHETIC STOP CODON IN FRAME WITH THE START CODON OF HSP CASSETTE ARE ALSO UNDERLINED.

FIG. 12

SYNTHETIC MULTIPLE CLONING SITE (MCS) + STRAND

GAA GGC GCG GCC GCG GTA CCA GAT CTT TAA ATC TAG ATA TCC ATG GAT
 CCA GCT GCA GAA TTC GAA GCT TAT CGA TGT CGACGT AGT TAA CTA GCG
 TAC GAT CGA CTG CCA GGC ATC AAATAA AAC GAA AGG CTC AGTCGA AAG
 ACT GGG CCT TTC GTT TTA TCT GTT TGT CCG GCC ATC ATG GCC GCG
 GTG ATC AGC TAG TAC G

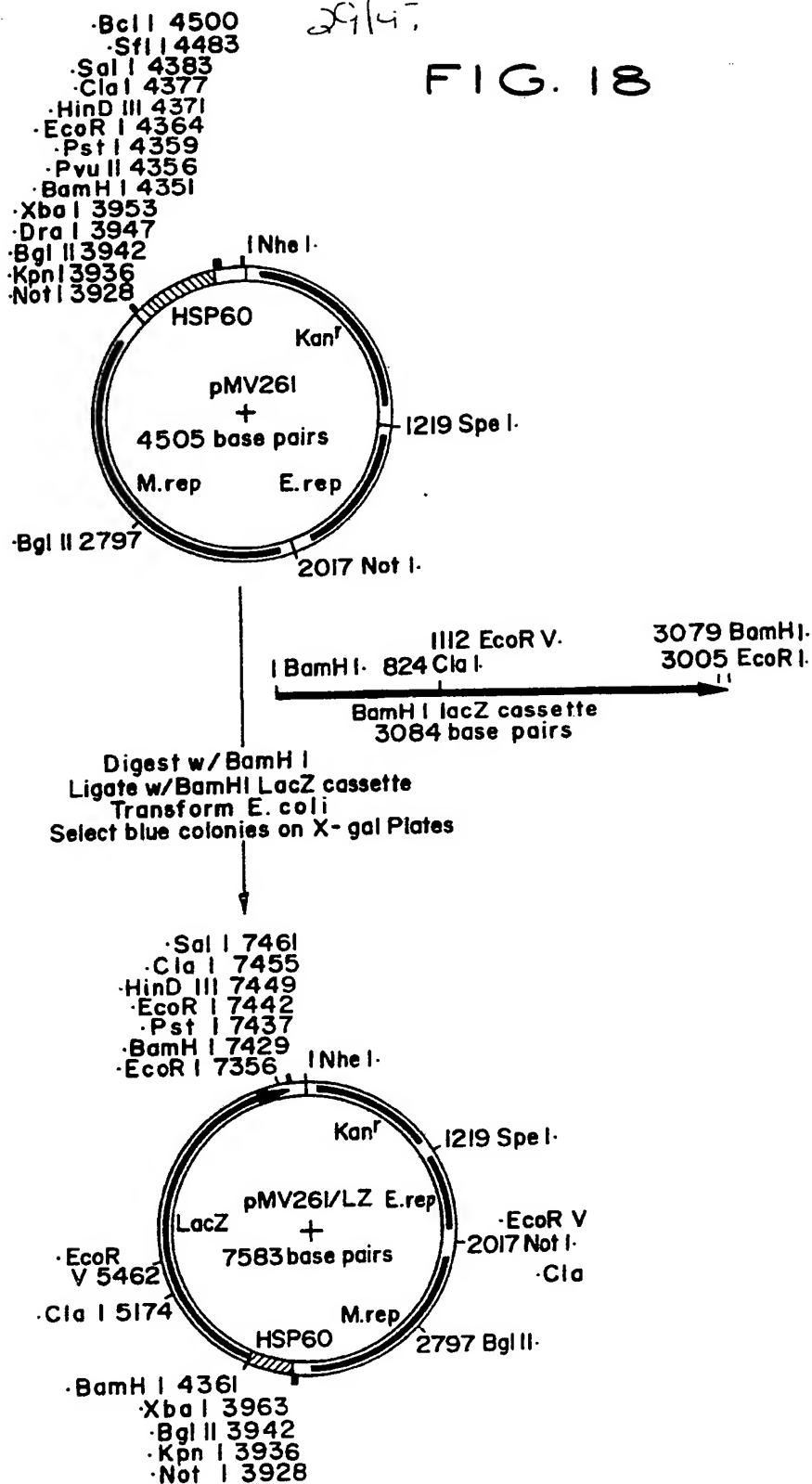


FIG. 19

AAAACACCCTCTGACCAGCGAGCGGGCGACGGGAATCGAAGCCGCGTAGCTAGTTTGGAAAGATGGGTGTCTGCCGACCACA attP
 AAAACACCCTCTGACCAGCGAGCGGGCGACGGGAATCGAAGCCGCGTAGCTAGTTTGGAAAGACTAGGGCTCTACCATTTGAGC attL
 CGCACGTGGCGGTCCCTACCGAGCGGGCGACGGGAATCGAAGCCGCGTAGCTAGTTTGGAAAGACTAGGGCTCTACCATTTGAGC attB

L5 BAM HI SITES

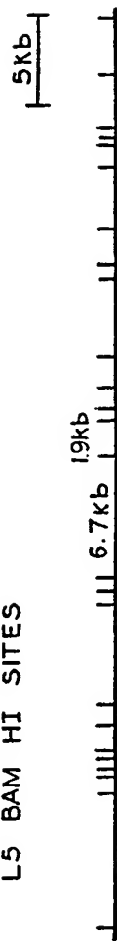
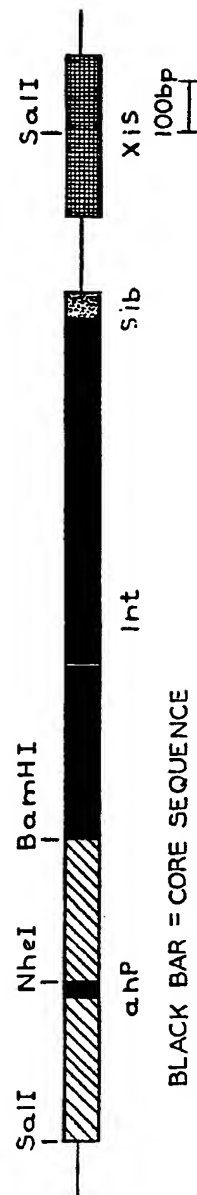


FIG. 21



BLACK BAR = CORE SEQUENCE

DOMAIN 1		DOMAIN 2	
INT (λ)	RLAMELAVVTGQRVGDLCEMKWSDIVDG	HELRLSA-RLYEKQ-ISKFAQHLLGHKS-DTMASQYR-	
INT (HK22)	RLAMD LAVVTGQRVGDLCEMKWSDIVDG	HELRLSA-RLYRNQ-IGDKFAQRLLGHKS-DSMAARYRD	
INT (480)	VFLVKFIMLTGCRTAERLSESWFRLD	HDMRRTIATNLSELG-CPPHVEKLLGHQM-VGVMAHYN-	
INT (P2)	KKIAILCLSTGARWGEAARLKAENIHN	HALRHSFATHFMING-GSITLQRILGHTR-IEQTMVYAH	
INT (P4)	MIAVKLSLLTFVRSSSELRFARWDEFDFD	HGFRTMARGALGESGLWSDDAIERQSLHSENNNVRAAYIH	
INT (P22)	KSVVEFALSTGLRRSNIINLEWQQIDMQ	HDLRHTWASWL VQAG-VPISVLQEMGWES- IEMVRRYAH	
INT (186)	ETVWRICLATGARWSEAESLRKSQLAKY	HVLRHTFASHFMMNG-GN ILVLQRVLGHTD- I KMTMRYAH	
INT (HP1)	GLIVR1CLATGARWSEAE TLTQSQVMPY	HVLRHTFASHFMMNG-GN ILVLKE ILGHST- IEMTMRYAH	
INT (L54a)	AGAVEVQALTGMRI GELLALQVKDVLK	HTLRHTHISLLAEMN- ISLKAIMKRVGHRDEKTTIKVYTH	
Cre (P1)	TAGVEKALSLGVTKLVERWISVSGVADD	HSARVGAARDMARAG-VSIP EIMQAGGWTN-VNIVMNYIR	
D Prot. (F)	KMLLATLWNTGARINEALALTRGDFSLA	HTFRHSYAMHMLYAG- IPLKVLQSLMGHKS- I SSTEVEYTK	
Fim B	YCLTLCCF IHGFRASEICRLRISDIDLK	HMLRHSCGFALANMG- IDTRL IQDYL GHRN- IRHTVRYTA	
Fim E	YCLILLAYRHGMRISELLDLHYODLDLN	HMLRHACGYELAERG-ADTRL IQDYL GHRN- IRHTVRYTA	31/47
Th2603 ORF3	RLFAQLLYGTCMRI SEGLQLRVKDLDFD	HTLRHSFATALLRSG-YD IRTVQDLLGHSD-VSTTMIYTH	
Th554 ThpA	KLILMLMYEGGLRIGEVLSRLIEDIVTW	HMLRHTHATQLIREG-WDVAFVQKRLGHAHVQTLNTYVH	
Th554 ThpB	ATMTMIVQECGMRI SELCTLKKGCLLED	HAFRHTVGTRMINNG-MPQHI VQKFLGHES-PEMFSRYAH	
Th4430 Thp1	YAIATLLAYTGVRISEALS IKMNDFNLQ	HQLRHFFCTNAIEKG-FS IHEVANQAGHSN- IHTTLLYT-	
Rci	YVIFHLALETAMRQQEILALRWEHIDL R	HDLRHEAISRFFELGSLNVMEIAA I SGHRS-MNMLKRYTH	
Th1545 ORF2	YDEILILLKTGLRISEFGGLTLPDLDFE	HIGRHLMTSFLSMKGLTELTVVGNWSDKRASAVATTYTH	
Flp	-----	HIGRHLMTSFLSMKGLTELTVVGNWSDKRASAVATTYTH	
CONSENSUS	--LV-L-)-TGmR-SEI--Lr--di---	H-LRHt-At-L----G---i---iQ-ILgh---i---T---Y-H	
L5	RI AAYILA WTSLSRFGELIELRRKDIVDD	HDLRAVGATFAAQAG-ATTKELMARLGHTT-PRMAMKYQM	

FIG. 20

32147
FIG. 22B

MATCH WITH FIG. 22A

CAGCTCGCTGAGAGCGGTGAAOGACAGGGGGAACGCCAGCCGCGCGAOG
+.....+.....+.....+.....+ 100
 GGTCGAGCGACTCTCGGCACTTGCTGTCCCGCTTGCGGTTCGGGCGCTGC
 ICTCTTCACTGCACCAGCTCCAATCTGGTGTGAATGCCCTTCGTCTGTTC
+.....+.....+.....+.....+ 200
 GAGAAGTGACGTGGTTCGAGGTAGACCACACTTACGGGGAGCAGACAAG
 .GGGATGCGTTGCAACCGOGTATGCCAGGTGAGAAGAGTCGCACAAGAG
+.....+.....+.....+.....+ 300
 TCCCTACGCAACGTITGGCGCATACGGGTCCAGTCTTCTCAGCGTGTCTC
 CCAGCGGAGCGGGCGACGGGAATCGAACCOCCTAGCTAGTTTCGAAGAA
+.....+.....+.....+.....+ 400
 VGTGCGCTCGCCCCGTGCCCTTAGCTTGGCGGCATCGATCAAACCTTGT
 all P core
 CTCGGCTGCATCCTCTAAGTGGAAGAAATTGCAGGTTCGTAGAAGCCGC
+.....+.....+.....+.....+ 500
 AGAGCCGACGTAGGAGATTACCTTTCTTTAAGTCCAGCATCTTCGCGC
 GAGAGGAGACCTAGTTGGCAACGTCCGGATGGGGATCCGTGAAGACTC
+.....+.....+.....+.....+ 600
 GCTCTCCTCTGGATCAACCGTGCAGCGCCTACCCCTAGCGACTTCTGAG
 PsiI
 I
 GGTACTACGCGCTGCAGACCTACGACAACAAGATCGAOCGCCGAA GCCTG
+.....+.....+.....+.....+ 700
 CCATGATGCGCGACGTCTGGATGCTGTTGTCTACCTGCGGCTTCGGAC
 Y Y A L Q T Y D N K M D A E A W
 Int start?
 ACCGGGCGAAGAAGGCAGCCGCCAGCGCCATCACGCTGGAGGAGTAC
+.....+.....+.....+.....+ 800
 CCTGGCCCCGTTCTTCCGTCCGGCGGTTCGGGTAGTGCACCTCCTCATG
 D R A K K A A A S A I T L E E Y
 TACAGCGGGCACGCGGAGCGCCCATCTACCCGGTGTCTAGGTGAAGTGG
+.....+.....+.....+.....+ 900
 ATGTCGCCCCGTGCGCCTCGCGGCGTAGATGGGCCACGATCCACTTCACC
 Y S G H A E R R I Y P V L G E V A
 GTAGGAAGCACCOCGACTGCCCGCCGGCATGCCTACAAOGTCTCCGGGC
+.....+.....+.....+.....+ 1000
 ATCCTTCGTGGGCTGACGGGCGGCGGTACGGATGTTGCAGGAGGCCCG
 R K H P T A R R H A Y N V L R A
 ATCGAGCAGAAGGCAGCCGATGAGCGCGAOGTAGAGGCGCTGAOCCT
+.....+.....+.....+.....+ 1100
 TAGTCTGTCTTCCGTCCGCTACTCGCGCTGCATCTCCGCGACTGCGGA
 I E Q K A A D E R D V E A L T P
 CATACTCCTGGCGTGGACGAGCCTCCGGTTCGGAGAGCTGATCGAGC
+.....+.....+.....+.....+ 1200
 GTATGTAGGACCGCACCTGCTCGGAGGCCAAGCCTCTCGACTAGCTCG
 Y I L A W T S L R F G E L I E L
 GCCGTGGCGCTTCCCGCGTGGGGAACAAGATCGTTCGTTGGCAACGCCAA
+.....+.....+.....+.....+ 1300
 CGGCAACCGCGAAGGGCGCAACCCCTTGTCTAGCAGCAACCGTTGCGGTT
 R G A S R V G N K I V V G N A K

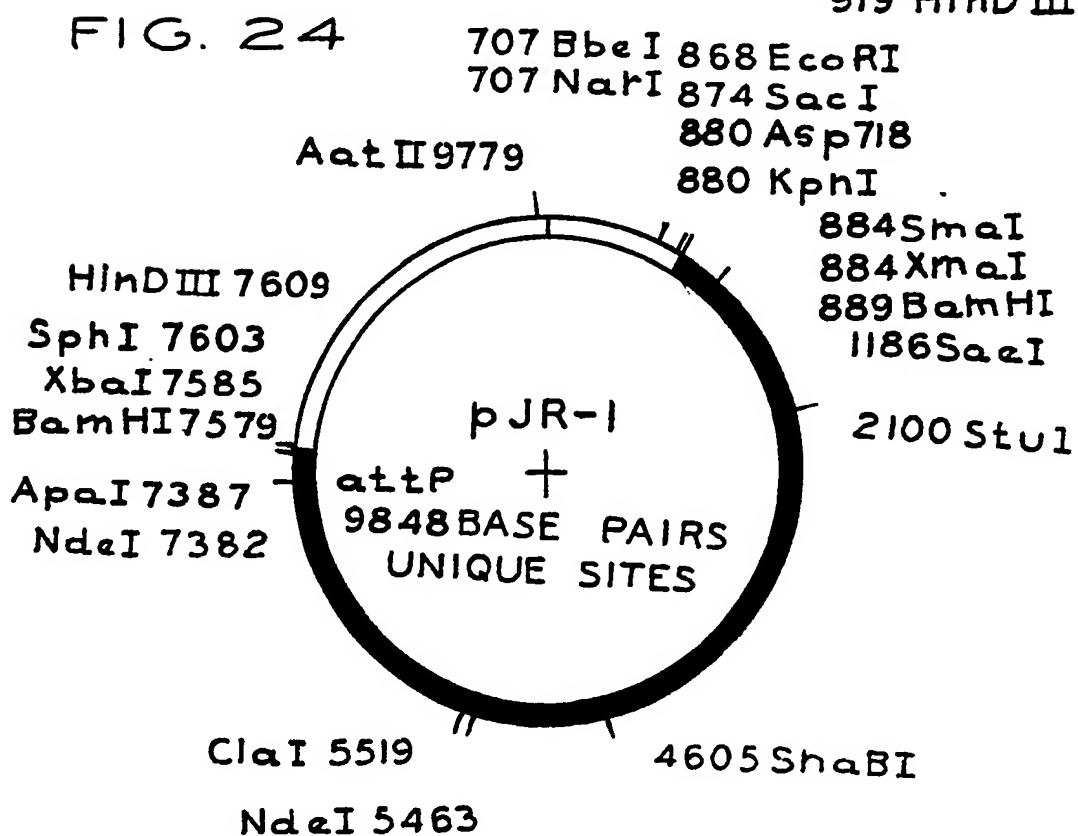
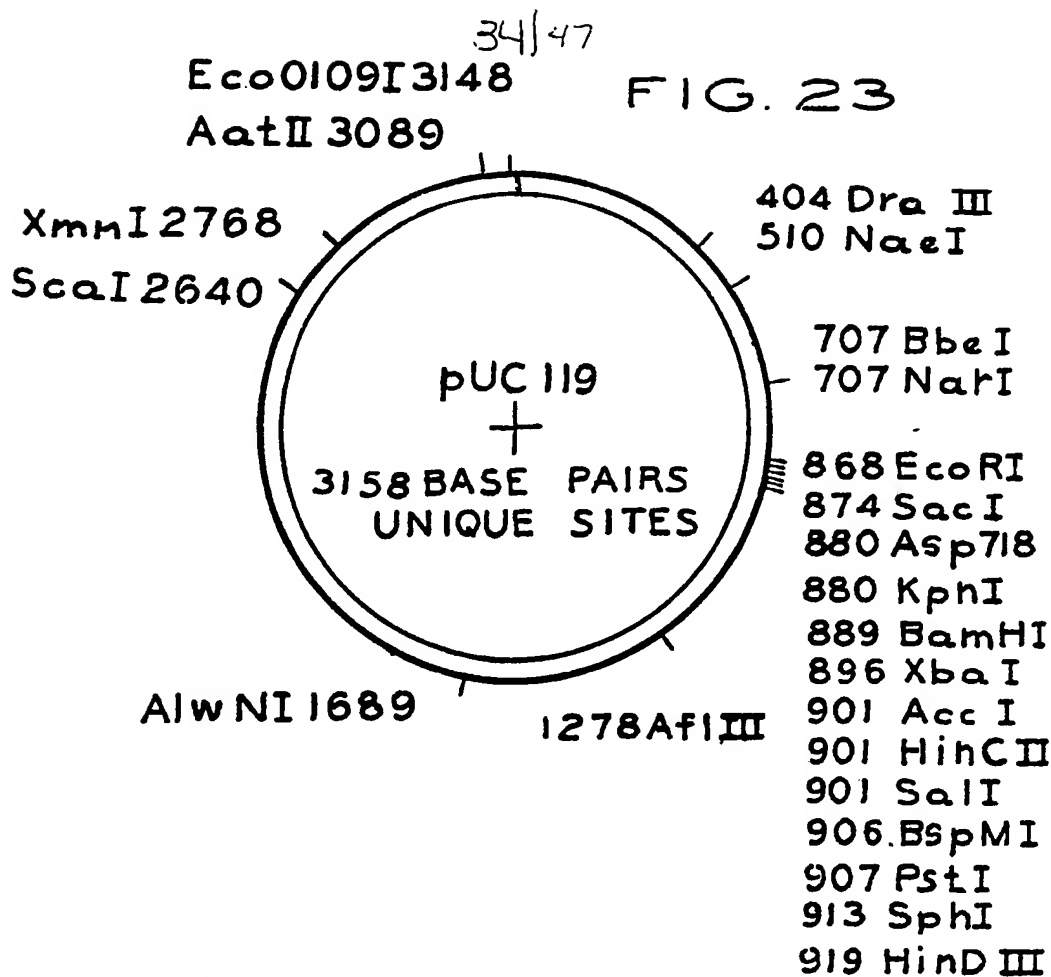
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FIG. 22A

1 GTCGACCACCAAGGGCAACATCTCTGCTTGGGCCACCCCGTIGGCCGAGC
-----+-----+-----+-----+-----+
CAGCTGGTGGTTCCCGTGGTAGAGACGAACCCCGTGGGGCAACCGGGCTC
101 GCGAGGGTTCCGACCGCTGCAACTCCCGGTGCAACCTTGTCCCGGTCTAT
-----+-----+-----+-----+-----+
CGCTCCAAGGCTGGCGACGTTGAGGGCCACGTTGGAACAGGGCCAGATAA
GCGCAGGCGGGGGGCTCTATTGCTTTGTACGATCGAAAGTAGCCAGATCA
201 -----+-----+-----+-----+-----+
CGCGTCCGCCCCCGAGATAAGCAAACAGTCGTAGCTTTCATCGGTCTAG
TTGCAGACCCCTGGAAAGAAAAATGGCCAGAGCGCGAAAAACACCCCTCTGA
301 -----+-----+-----+-----+-----+
AACGTCTGGGGACCTTTCTTTTACCGGTCTCCCGCTTTTGTGGGAGACT
Nde I
I
401 TGGGTGTCAGCCGACCACATATGGGCCGGTCAAGATAGGTTTTTACCCCT
-----+-----+-----+-----+-----+
ACCACAGACGGCTGGTGTATACCCGGCCAGTTCATCCAAAAAATGGGG
501 TTGAAGCCTGAGAGTTGCACAGGAGTTGCAACCCGGTAGCCTTGTTCACGAC
-----+-----+-----+-----+-----+
AACTTCGGACTCTCAACGTGTCTCAACGTTGGGCCATCGGAAACAAGTGCT
Bam III
I
601 AGCGCAGCGGGAGGATCCAAGCCTCATACGTCAACCCGACGGACGGTGTGA
-----+-----+-----+-----+-----+
TCGCGTCGCCCTCCTAGGTTCCGAGTATGCAGTTGGGCGTCTGCCACACT
Int
V R
Int start?
701 CGCGGGCGAGAAGCGGCTCATCGAGATGGAGACCTGGACCCCTCCACAGG
-----+-----+-----+-----+-----+
CGAGCGCCCGCTCTTCGCCGAGTAGCTCTACCCTGGGACCTGGGGAGGTGT
Int L A G E K R L I E M E T W T P P Q
801 ACCCGGAAGTGGCTCGTGGAGCGCGACCTCGCAGACGGCACCAGGGATCTG
-----+-----+-----+-----+-----+
TGGGCCTTCACCGAGCACCTCGCGCTGGAGCGTCTGCCGTGGTCCCTAGAC
T R K W L V E R D L A D G T R D L
901 CGGTACAGAGATGACGCCAGCTCTGGTCCGTGCGTGGTGGGCGGGATGG
-----+-----+-----+-----+-----+
GCCAGTGTCTCTACTGCGGTGAGACCACGCACGCACCACCGGCCCTACCC
V T E M T P A L V R A W W A G M G
1001 GGTGATGAACACAGCGGTGAGGACAAGCTGATCGCAGAGAACCCGTGCCGG
-----+-----+-----+-----+-----+
CCACTACTTGTGTGCCAGCTCCTGTTGCACTAGCGTCTCTTGGGCACGGCC
V M N T A V E D K L I A E N P C R
Bg III
I
1101 GAGGAGCTGGACATCGTCGCCGCTGAGATCTTCGAGCACTACCGGATCGCGG
-----+-----+-----+-----+-----+
CTCCTCGACCTGTAGCAGCGGCGACTCTAGAAGCTCGTGATGGCCTAGCGCC
E E L D I V A A E I F E H Y R I A A
TTGCCCGCAAGGACATCGTGGACGACGGCATGACGATGAAGCTCCGGGTGC
1201 -----+-----+-----+-----+-----+
AAGCGGCGTTCCTGTAGCACCTGCTGCCGTACTGCTACTTCGAGGCCACG
R R K D I V D D G M T M K I R V R

MATCH WITH FIG. 22B

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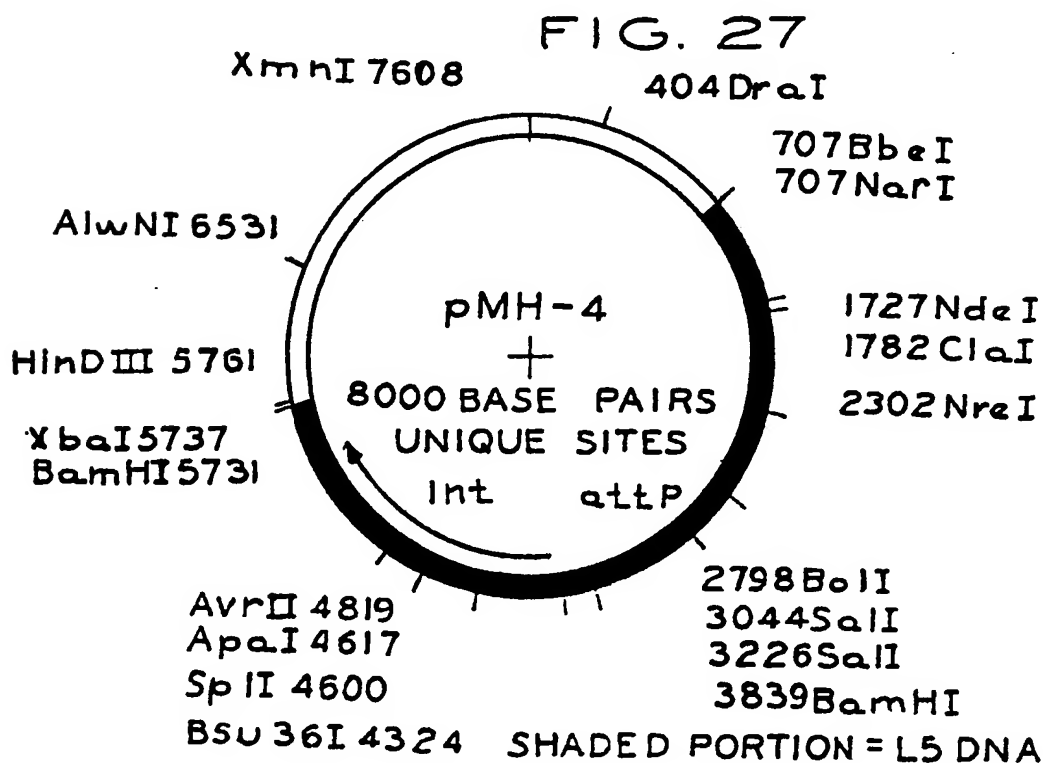
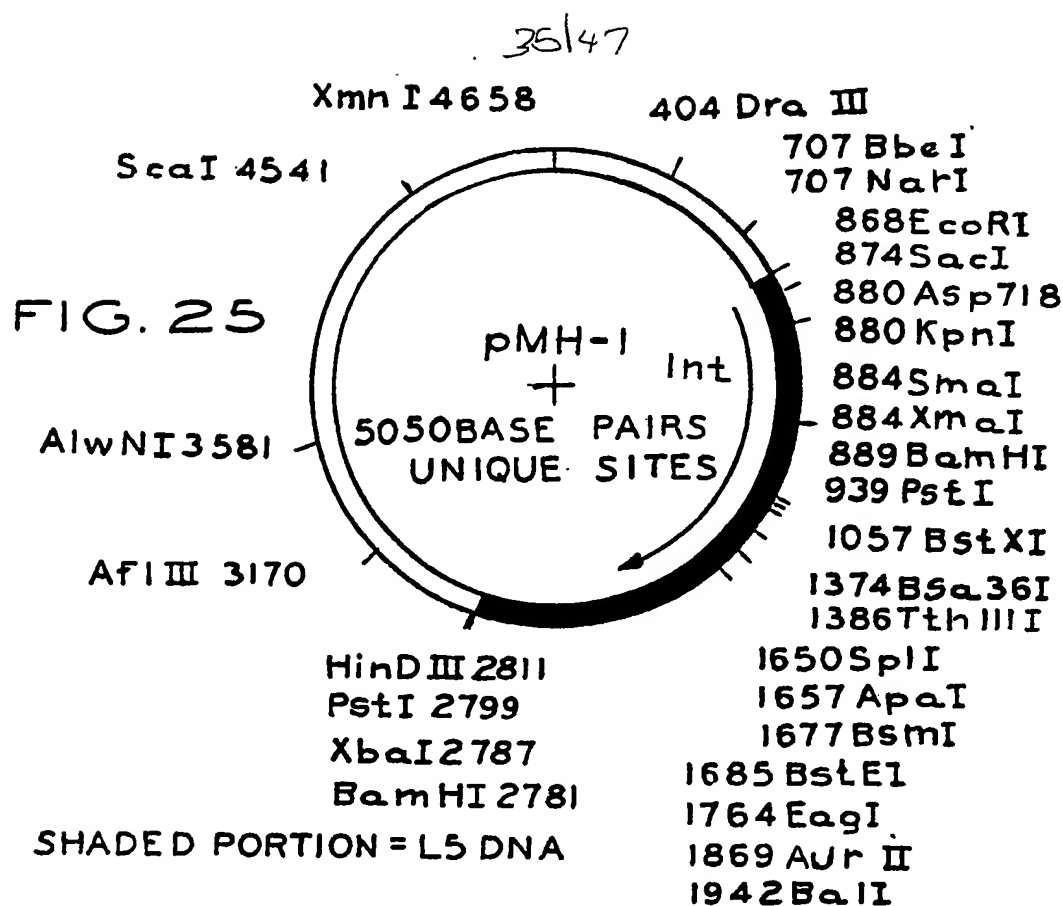


FIG. 28

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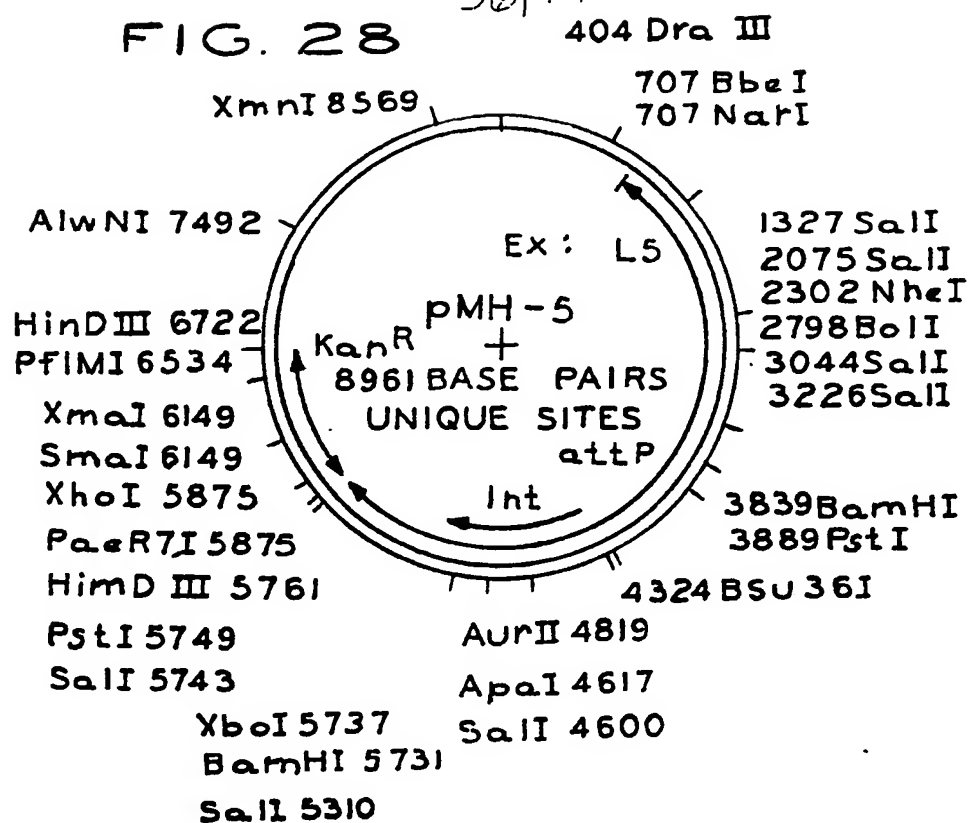
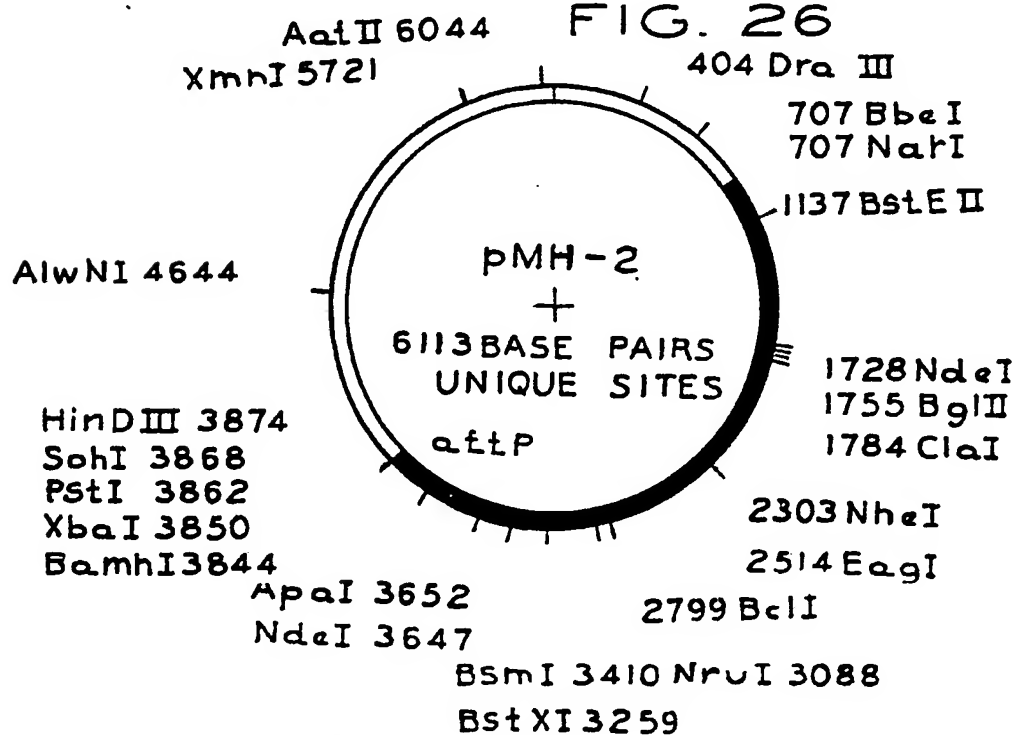


FIG. 26



SHADED PORTION = L5 DNA

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FIG. 29

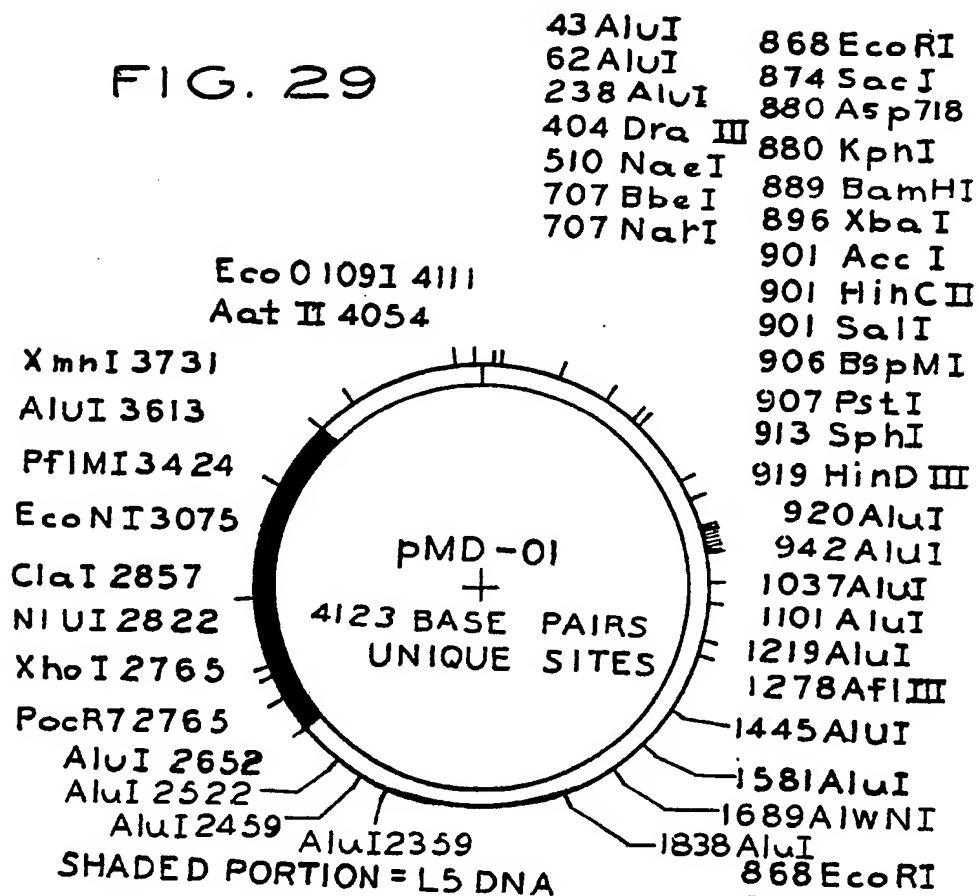
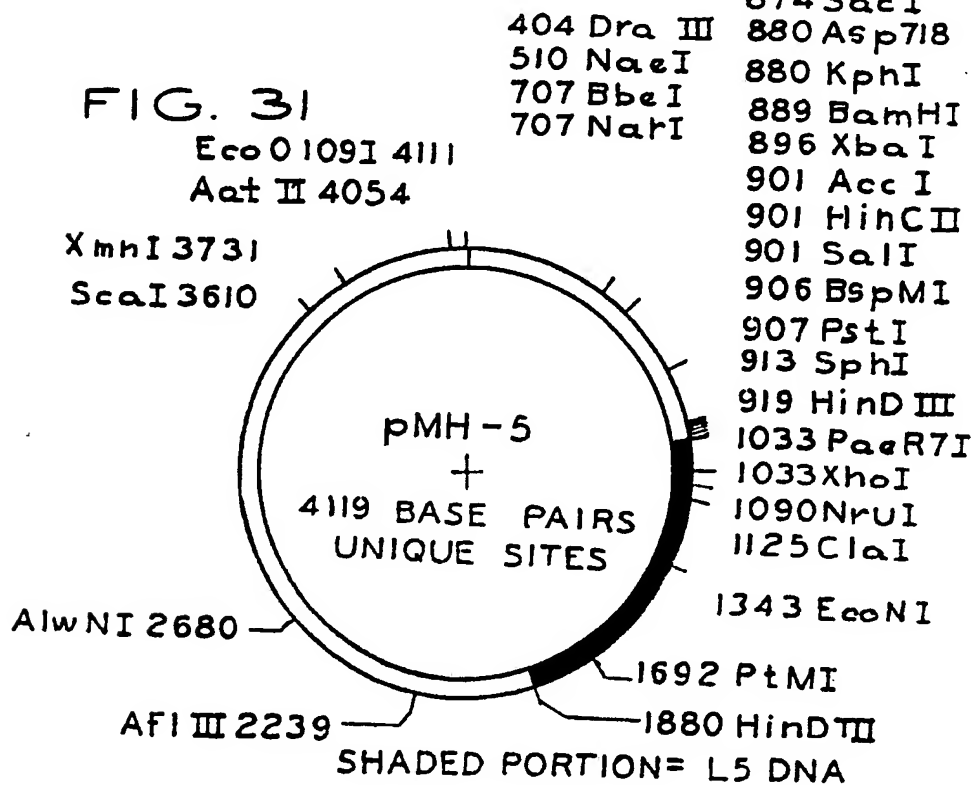
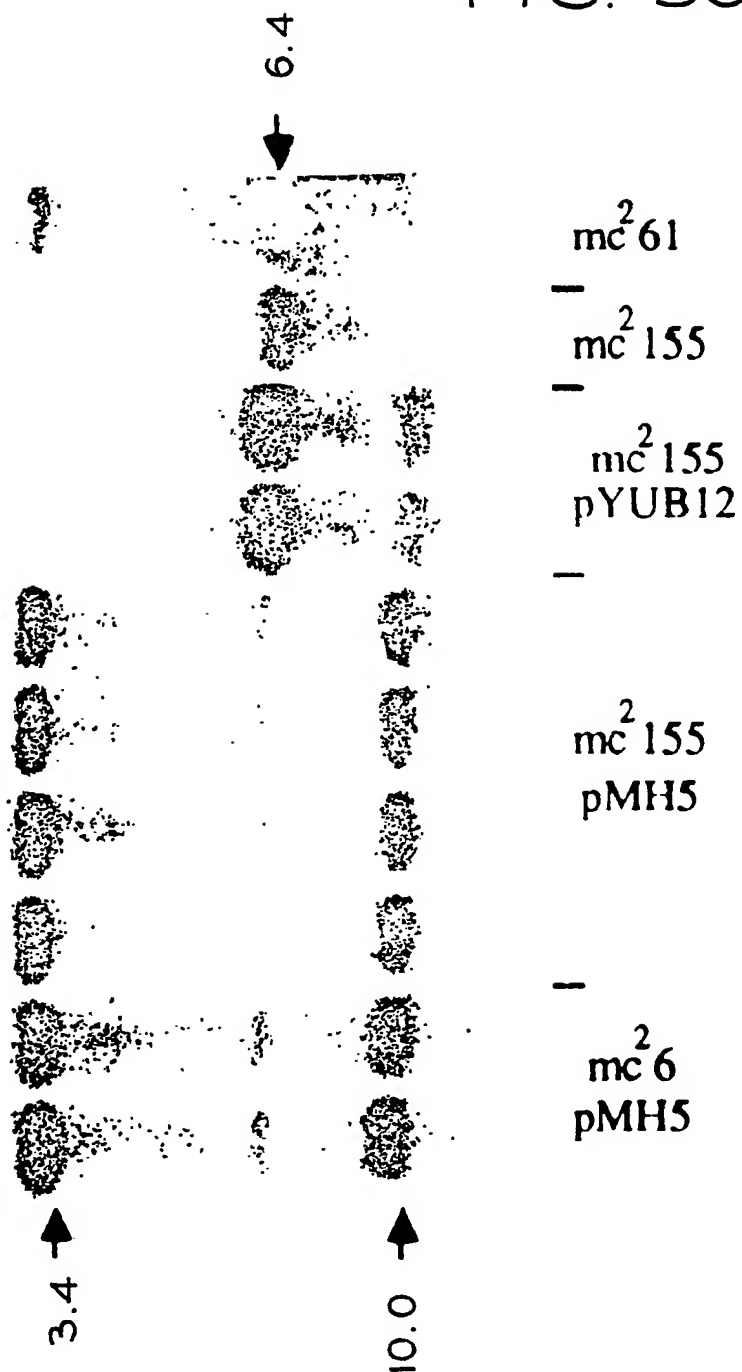


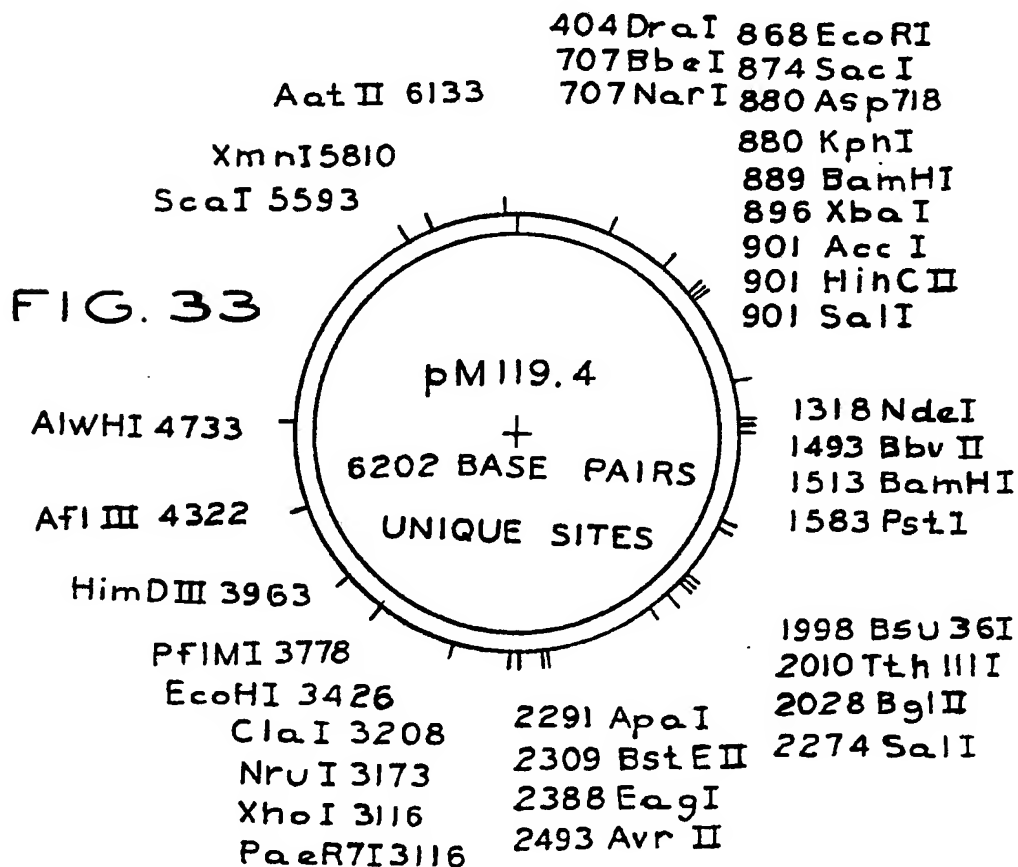
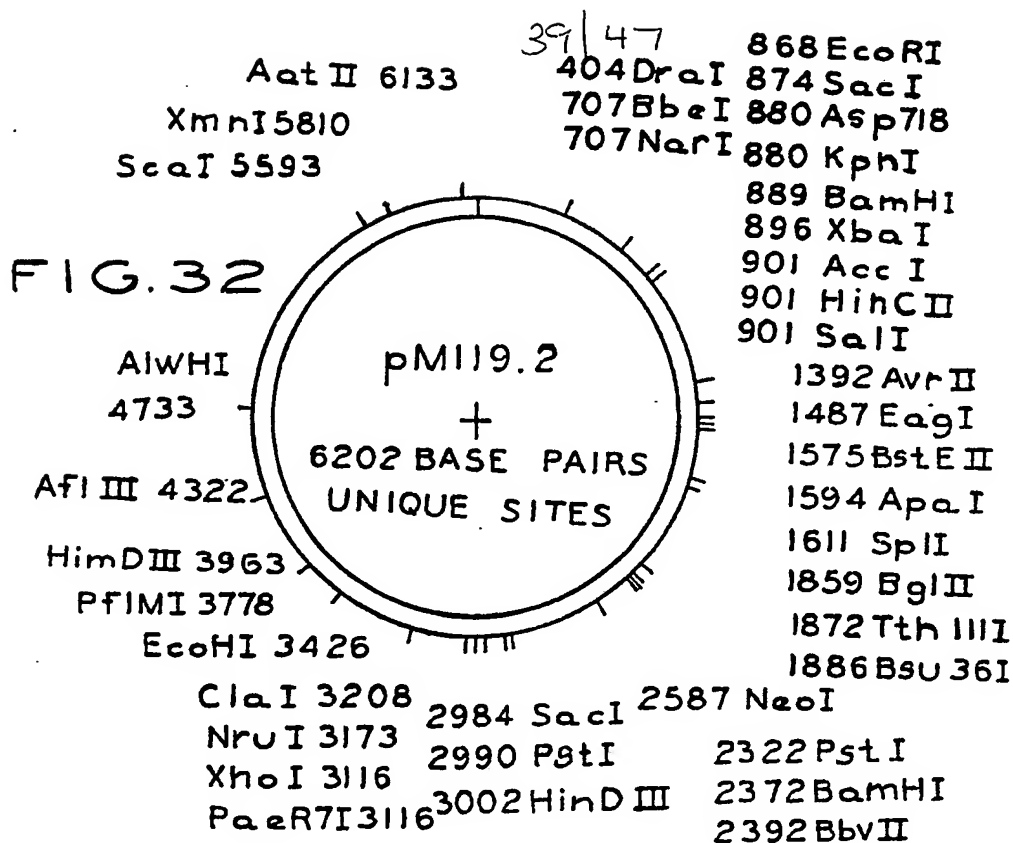
FIG. 31



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FIG. 30



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FIG. 34

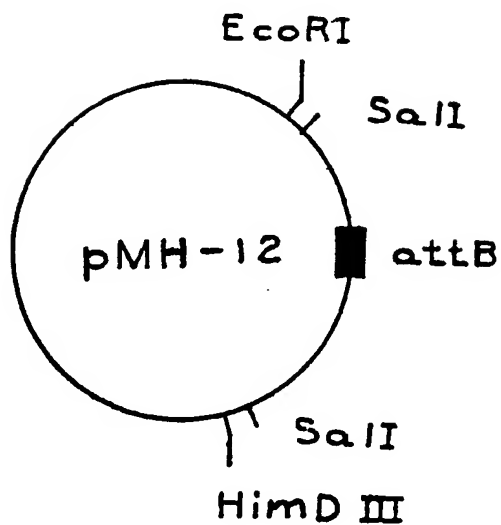
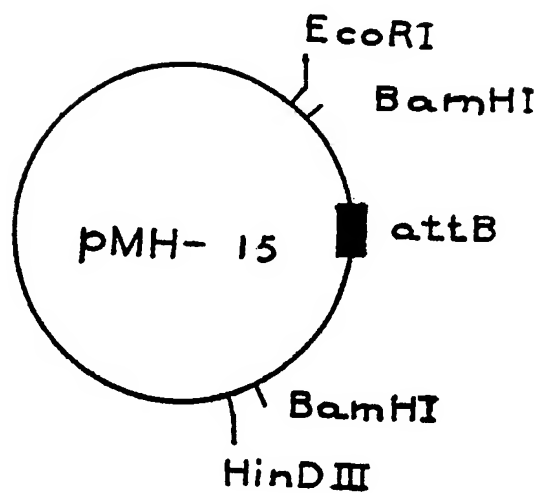


FIG. 36



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FIG. 37

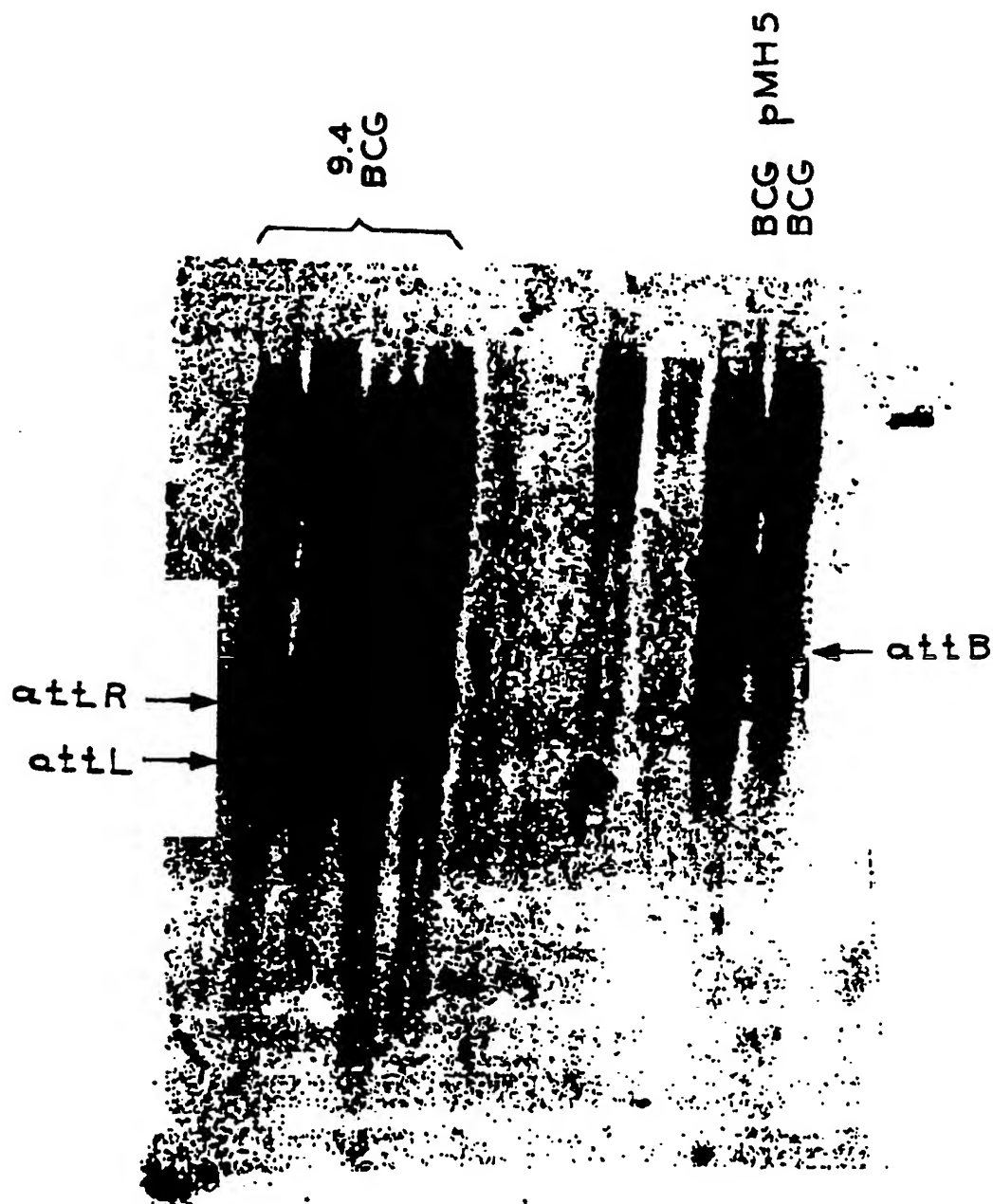
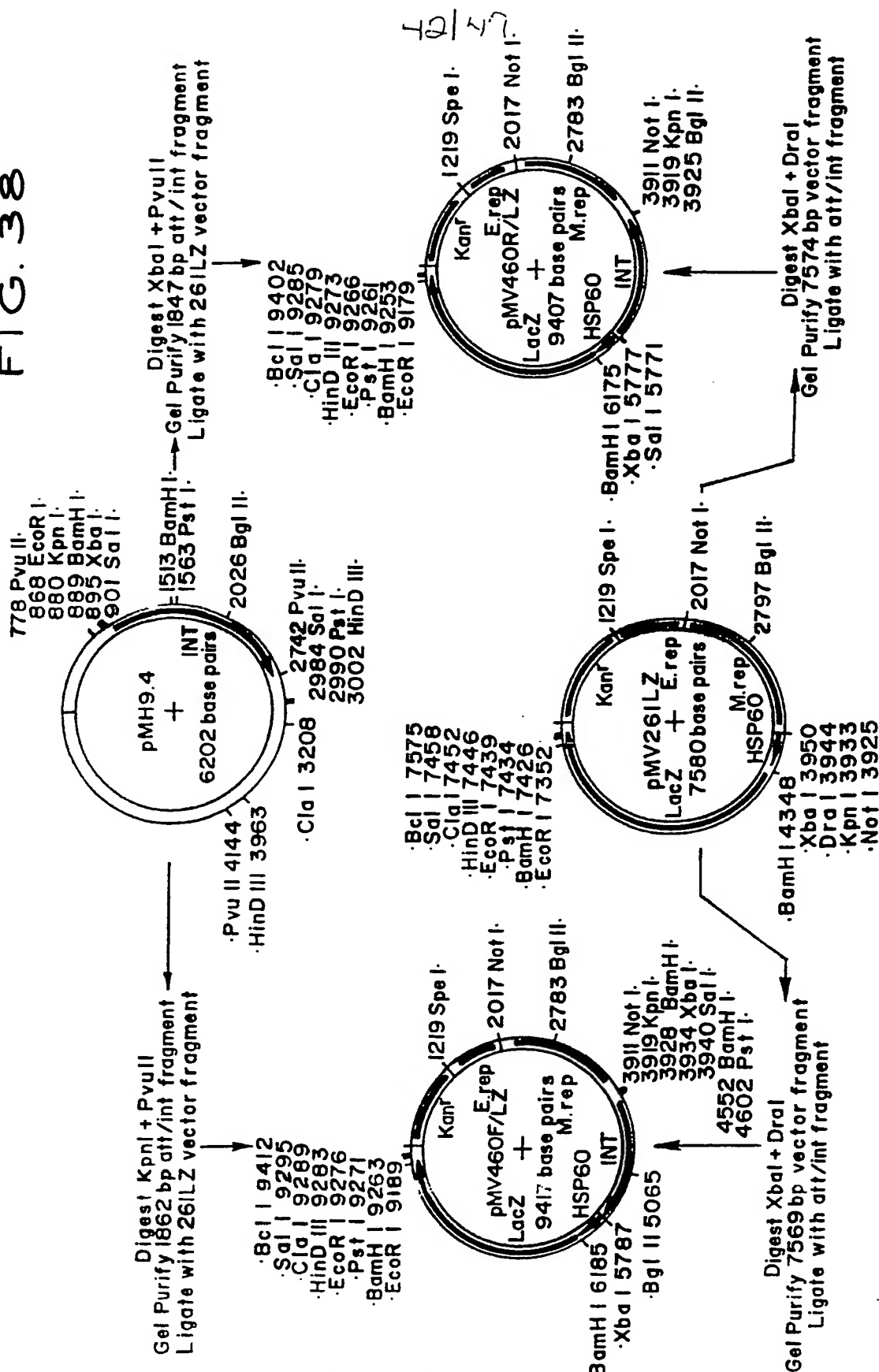
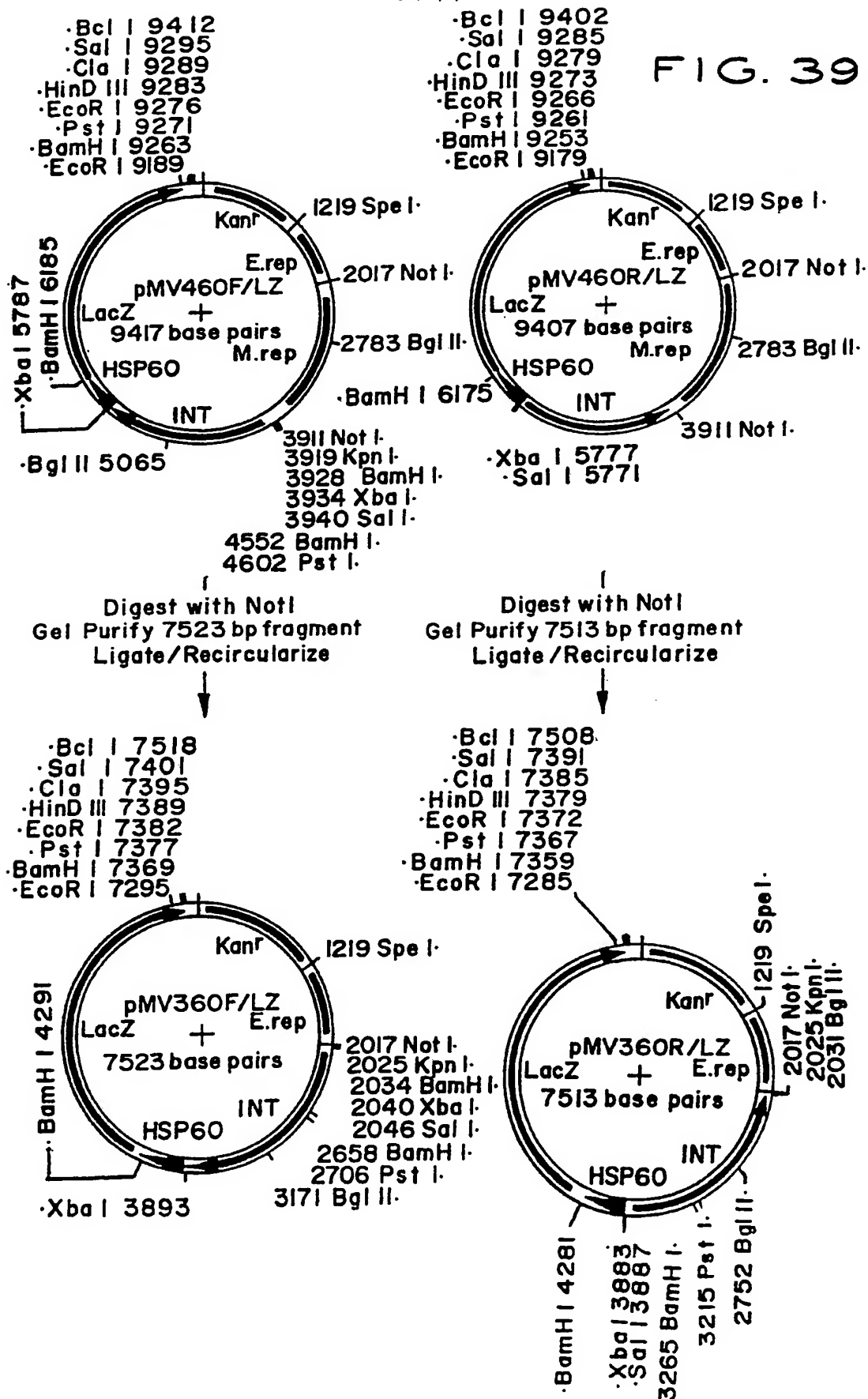


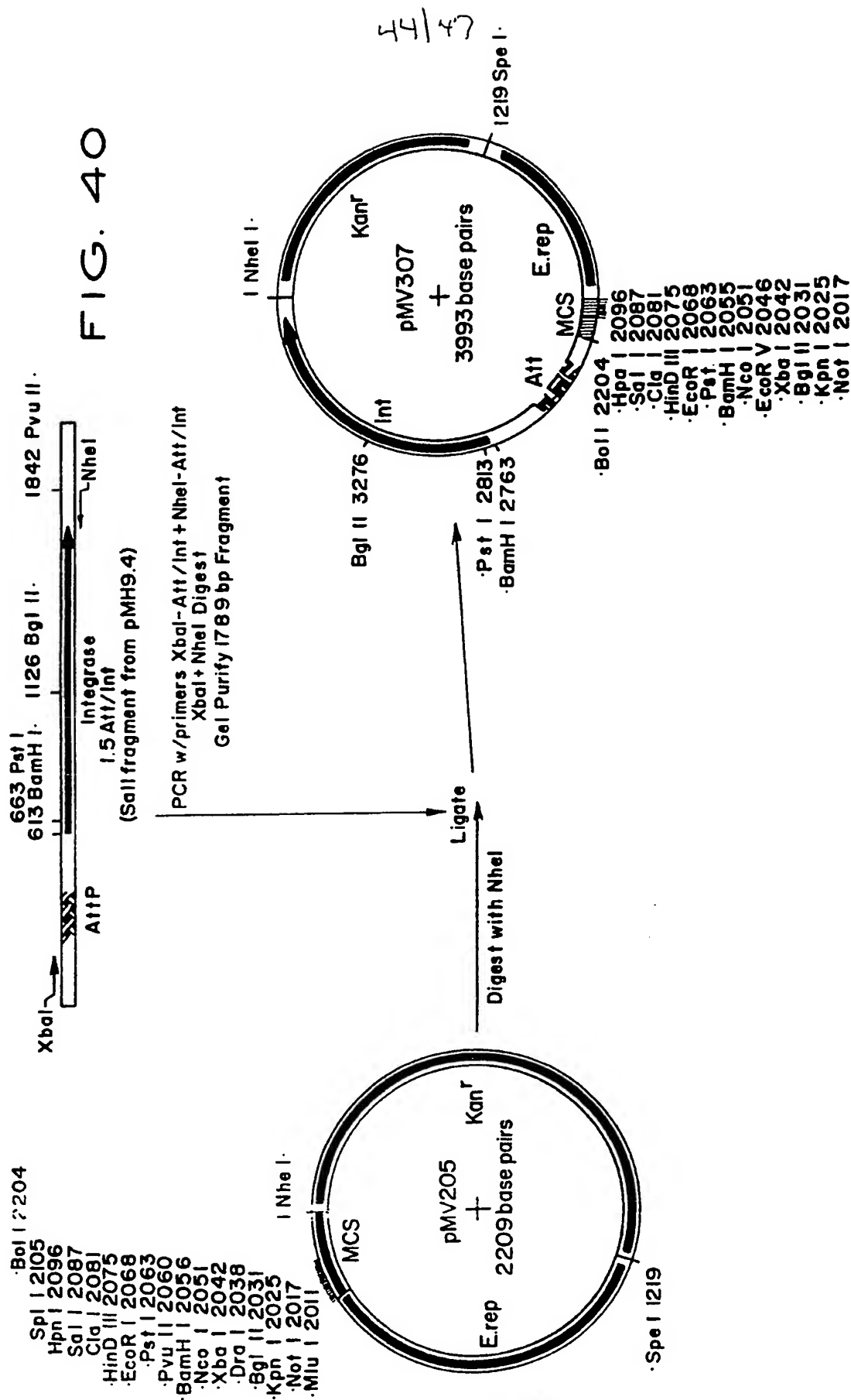
FIG. 38



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FIG. 39





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FIG. 44

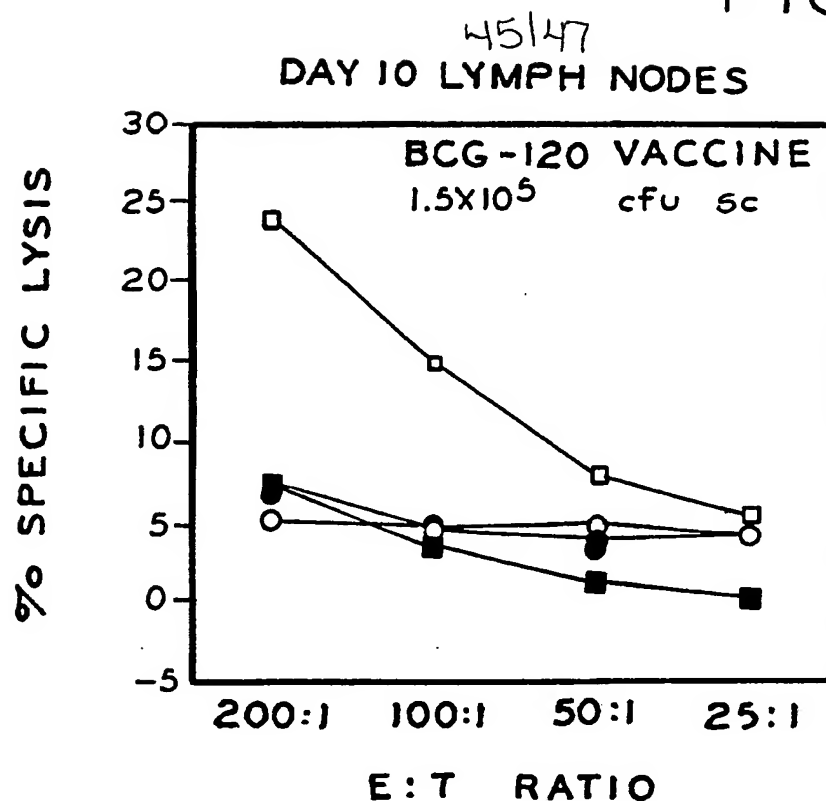
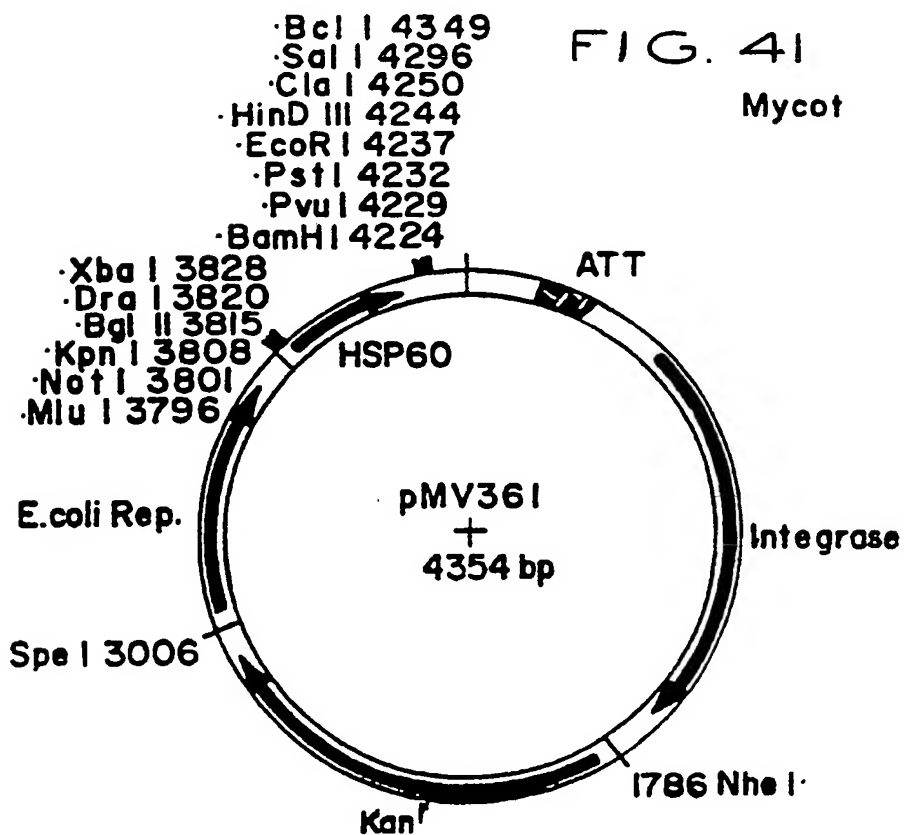


FIG. 41



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FIG. 35

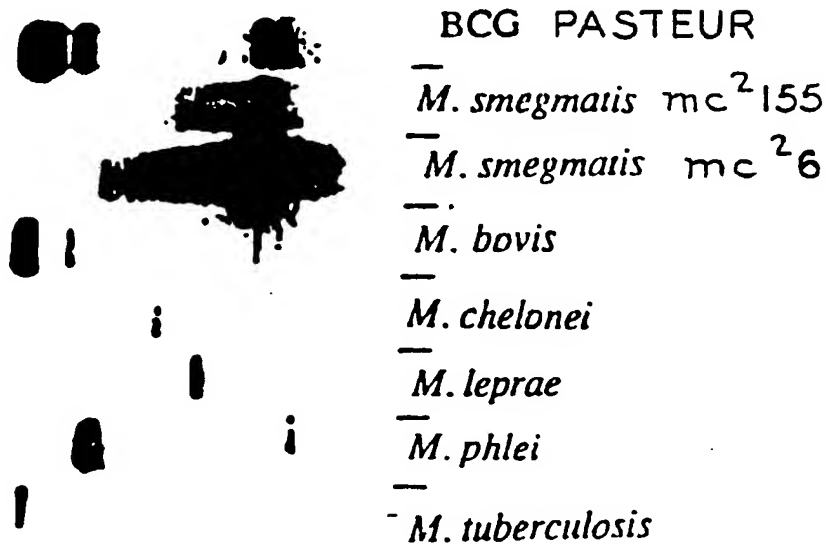


FIG. 42



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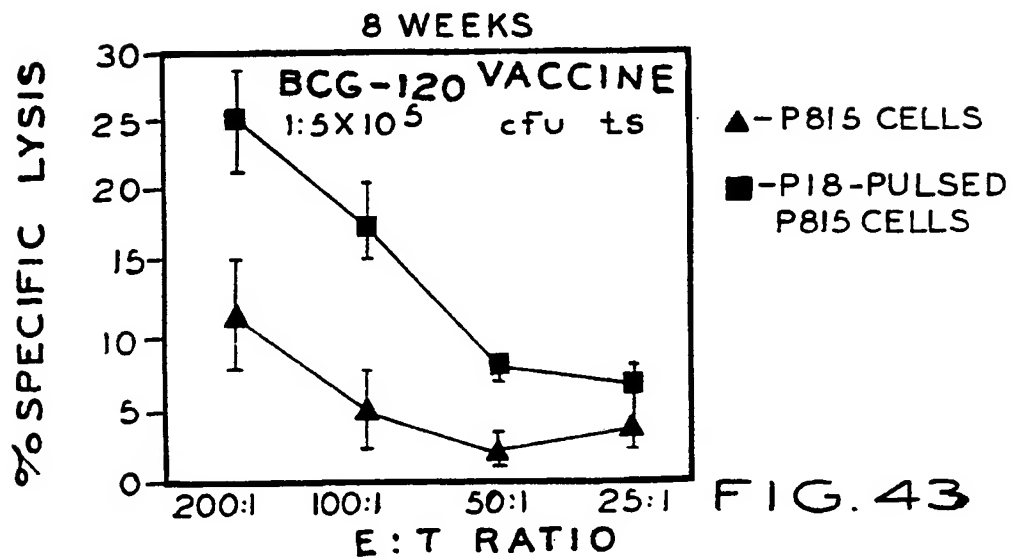
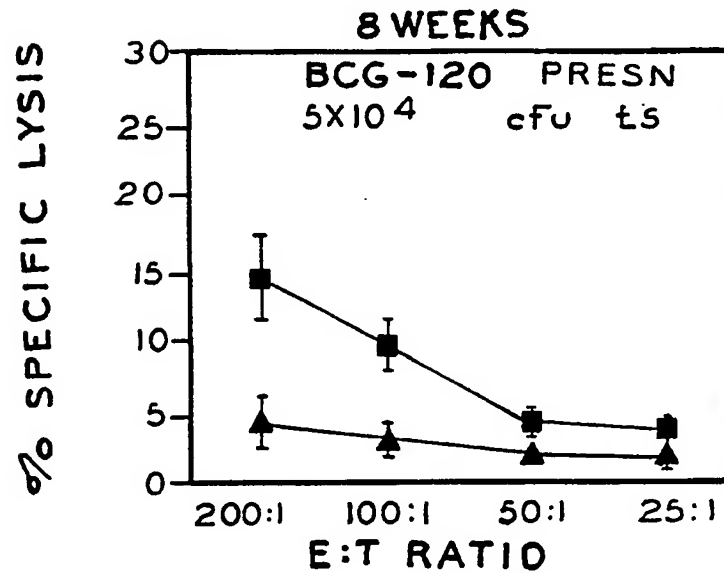
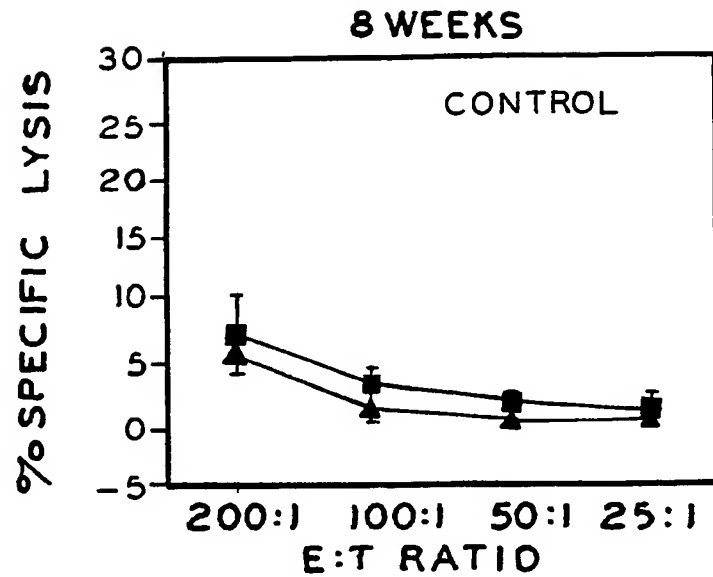


FIG. 43

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/04538

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :A61K 39/12

US CL :424/89; 435/863

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/89; 435/863

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS; Dialog (files = 155,154,5,399) (search terms: mycobacteria, vectors, HIV, recombinant)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 90/00594 (Bloom, et al) 25 January 1990, pages 1-95, especially pages 6, 11, 79, 81 and 92.	1-8
Y	Nature, Volume 328, issued 23 July 1987, Walker et al, "HIV-Specific cytotoxic T Lymphocytes In Seropositive Individuals", pages 345-348, see entire document.	1-8

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed	"G"	document member of the same patent family

Date of the actual completion of the international search

06 August 1992

Date of mailing of the international search report

13 AUG 1992

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